

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 20:22:24 ; Search time 6020 Seconds
(without alignments)
10622.738 Million cell updates/sec

Title: US-10-647-649-2

Perfect score: 1125

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5881141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vl.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	431.4	38.3	1280	15	AB027428 Oryza sat
2	431.4	38.3	1296	15	AK104862 Oryza sat
3	431.2	38.3	993	6	AX53028 Sequence
4	430.6	38.3	1141	15	AF001523 Musa acum
5	430	38.2	1261	6	AX006978 Sequence
6	427.2	38.0	1439	15	AF112967 Triticum
7	423.2	37.6	110000	15	AP008207_413
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9	422	37.5	1426	15	TABETGLUB
10	421.8	37.5	1041	15	AF004838
11	419.4	37.3	1295	15	AK070677 Oryza sat
12	418.2	37.2	1834	15	OSU72251
13	415.6	36.9	3559	6	BD080855 Banana pr
14	409.8	36.4	1249	15	AY612193
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16	393.6	35.0	1448	15	ASBGLUCAN
17	382.4	34.0	6260	15	HYBDG
18	380.8	33.8	4643	15	HVGLUEND

19	380.8	33.8	4849	15	HVGLB1
20	378.6	33.7	5159	15	BLYGLB2
21	370.2	32.9	1265	15	MZEL1BGLCN
22	368.2	32.7	1269	15	AF112965
23	364.8	32.4	1311	15	AY353062
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40	343	30.5	1257	15	HVU21367
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ALIGNMENTS

RESULT 1

AB027428

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDs

AB027428 Oryza sativa mRNA for beta 1,3-glucanase, complete cds,
clone:R1149.

AB027428 Oryza sativa mRNA for beta 1,3-glucanase, complete cds,
clone:R1149.

AB027428.1 GI:4884525
beta 1,3-glucanase.

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 1280)
Itoh, Y. and Sasaki, T.

Oryza sativa mRNA for beta 1,3-glucanase
Published Only in Database (1999)

2 (bases 1 to 1280)
Itoh, Y. and Sasaki, T.

Direct Submission
Submitted (17-MAY-1999) Yoshifumi Itoh, National Food Research
Institute, Applied Microbiology; Kannondai 2-1-2, Tsukuba, Ibaraki
305-8642, Japan (E-mail: yosifumi@nri.affrc.go.jp,
Tel: +81-298-38-9075, Fax: +81-298-38-7996)

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polyA_signal
polyA_signal
polyA_site
ORIGIN

Query Match 38.3%; Score 431.4; DB 15; Length 1280;
Best Local Similarity 66.8%; Pred. No. 3.4e-75;
Matches 682; Conservative 0; Mismatches 321; Indels 18; Gaps 4;
/note="30 A nucleotides"

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146 GCATTCCTACAGTGGTCAATCTATCGCGTGTCTACGGCGTGTATCGGGAACAACCTG 205
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Db 1031 TTGCGGCTTCAACCCCGGACGAGTCCGCGGATCTCCATCAATTTCTAAGAAGATTGT 1090

Qy 1024 T 1024
Db 1091 T 1091

RESULT 2
AK104862
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE

AK104862 1296 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:001-043-E09, full
insert sequence.
AK104862
AK104862.1 GI:32990071
FLI_CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otomoto, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Oato, N., Oka, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice

2 (bases 1 to 1296)
12869764
japonica rice
Science 301 (5631), 376-379 (2003)

JOURNAL
PUBMED
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Komoto, H., Kouda, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Naniki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
Oato, N., Oka, Y., Otomo, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, P., Takaku-Akashira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
Yoshimura, A.

TITLE
JOURNAL

Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of

Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skkuchien@ias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica rice.

COMMENT

URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

PAIS Genome Sequencing & Analysis Group: Otono, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J., Mizuno, K., Narioka, K., Niihara, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsuura, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Kato, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES

source

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ORIGIN

Query Match 38.3%; Score 431.4; DB 15; Length 1296;
Best Local Similarity 66.8%; Pred. No. 3.4e-75;
Matches 682; Conservative 0; Mismatches 321; Indels 18; Gaps 4;
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RESULT 3
AX653028
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DEFINITION Sequence 2898 from Patent WO03000898.
ACCESSION AX653028
VERSION AX653028.1 GI:29155842
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 2898 03-JAN-2003;
SYNOPSIS Syngenta Participations AG (CH)
FEATURES
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/organism="Oryza sativa"
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ORIGIN

Query Match 38.3%; Score 431.2; DB 6; Length 993;
Best Local Similarity 67.2%; Pred. No. 3.7e-75;
Matches 677; Conservative 0; Mismatches 313; Indels 18; Gaps 4;

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604 TACTTGAGTATGTGCAACTCCGGATCCATCGACCTCTCATACGCGCTCTTACTGCA 663
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
583 TACTTCGCTACGTGGGCAACAGGCCAGATCGACATCACTAGCGCTCTTCACTG 642
664 TCTGTCAGTGTGTCAGGAGCGGTCTTACGCTTACAAACCTTTCGATGCCATGTC 723
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703 GACAGCTTCTACTCGGCTGGAGAGCGCGGCGCGGCGGCGTCCCGATCGTGTGTGTCG 762
784 GAGAGTGTGCTGCGCTGACGCGGGGAGACGCGGAGCGGTGTCTAATGCGCAGACTTAC 843
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763 GAGAGCGGTGCGCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 822
844 AATTCCAAATTTGATCAACCATGTGGTTCAGGGGAGCGCGGAGGCGGCGGCGGCGGCGG 903
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823 AACCAGAACCTGATCAACCATGTCGGGAGGAGCGCGGCAAGAGAGCGCGGCGGAGCATCGAG 882
904 ACCTACATTTGCGATGTTCAACGAGATCAGAGCAGCGCGGAGGCGGAGGATGAGATTAAC 963
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943 TTCGCGCTTTCACCCCGGACGATCGCGGCGGCTACTCTCATCAATTTC 990
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RESULT 4
AF001523 1141 bp mRNA linear PLN 21-MAR-2000
LOCUS Musa acuminata beta-1, 3-glucanase mRNA, complete cds.
DEFINITION

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ACCSSION AF001523
VERSION AF001523.2 GI:6073859
KEYWORDS .
SOURCE Musa acuminata
ORGANISM Musa acuminata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.
REFERENCE 1 (bases 1 to 1141)
AUTHORS Clendennen,S.K. and May,G.D.
TITLE Differential gene expression in ripening banana fruit
JOURNAL Plant Physiol. 115 (2), 463-469 (1997)
PUBMED 9342866
REFERENCE 2 (bases 1 to 1141)
AUTHORS Peumans,W.J., Barre,A., Derycke,V., Rouge,P., Zhang,W., May,G.D.,
Delcour,J.A., Van Leuven,E. and Van Damme,E.J.
TITLE Purification, characterization and structural analysis of an
abundant beta-1,3-glucanase from banana fruit
JOURNAL Eur. J. Biochem. 267 (4), 1188-1195 (2000)
PUBMED 10672030
REFERENCE 3 (bases 1 to 1141)
AUTHORS Clendennen,S.K. and May,G.D.
TITLE Direct Submission
JOURNAL Submitted (29-APR-1997) Plants and Human Health, Boyce Thompson
Institute for Plant Research, Tower Rd., Ithaca, NY 14853, USA
REFERENCE 4 (bases 1 to 1141)
AUTHORS Van Damme,E.J., May,G.D. and Clendennen,S.K.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1999) Lab. Phytopathology and Plant Protection,
K. U. Leuven, Willem de Croylaan 42, Leuven B 3001, Belgium
REMARK Sequence update by submitter
COMMENT On Oct 20, 1999 this sequence version replaced gi:2586138.
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TGVLGTSYPPSAGAFSSAAQAYLSPIVQFLASNGAPLLVNVYPYPSVTGNPGQISLVP
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VYQISF"
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Best Local Similarity 67.0%; Pred. No. 4.8e-75;
Matches 706; Conservative 0; Mismatches 329; Indels 18; Gaps 6;
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QY 64 GCAATCCCGAGAGCGGTGGAATCCATTGGGTCTGCAATGGAATGGAGCGGTGACAACTTC 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GCAGTTCCAAACAGAGTGCATCGATTGGTGTCTGTCTACGCGATGCTCGGCAACAATCTT 120
QY 124 CCCAGCCCGCGGAGCGCTGTCACCTCTACAGTCCCAACATAGCTGGCATCGGACTC 183
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 CCCCCCGCGGAGCGGTGTCAGTCTCTTACAAATCCCAACATCGCGAGATGAGATC 180
QY 184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGCTCTAAACATCTACTCTCCTC 243
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TACGATCCAAACCAAGCGCGCTCGAGCCCTCAGAACTCCAACTCCAACTCTCTGTTG 240
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QY 894 --GGCGATTGAGCCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCGCGAAGGG 951
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RESULT 6

AF112967 1439 bp mRNA linear PLN 06-MAY-2002
 LOCUS Triticum aestivum beta-1,3-glucanase precursor (Glb3) mRNA,
 DEFINITION complete cds.

ACCESSION

AF112967

VERSION

AF112967.1 GI:4741849

KEYWORDS

SOURCE

ORGANISM

Triticum aestivum (bread wheat)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1. (bases 1 to 1439)
 Li, W., Faris, J.D., Muthukrishnan, S., Liu, D., Chen, P. and Gill, B.S.
 Isolation and Characterization of cDNA Clones of Acidic Chitinases
 and beta-1,3-Glucanases from Wheat Spike Induced by Fusarium
 graminearum

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

ORIGIN

Query Match

Best Local Similarity

Matches 656; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY

Db

21

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RESULT 7

AP008207_413

WPCOMMENT

Sequence split into 433 fragments

LOCUS AP008207

Accession AP008207

Fragment Name

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End

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AP008207_001

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310000

AP008207_002

200001

310000

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AP008207_192	19200001	19310000	
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AP008207_194	19400001	19510000	
AP008207_195	19500001	19610000	
AP008207_196	19600001	19710000	

Query Match	37.6%	Score 423.2;	DB 15;	Length 110000;
Best Local Similarity	67.6%	Pred. No. 1.5e-73;		
Mismatches	644;	Conservative	0;	Mismatches 293; Indels 15; Gaps 3;

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Qy	133	GCCGACGTGTCAACTCTTCAAGTCCAAACATAGTGGCATGCGACTCTACAGCCCC	192
Db	39664	AGCGACGTGTGTCAGCTCTTCAAGTCCAAACGCGCATCGACTCCATGCGCATCTACTTCCCA	39723
Qy	193	GACCAAGCCACTCTCCAGGCGCTTCAGGCTCTTACATCTACCTCATCTCTCGAGTCCCC	252
Db	39784	AGAAGCGATCTCTCCAGGCGCTTACGCGCTCAAGCTCGCGCTCACCATGAGCGTGGC	39783
Qy	253	AACTCGACCTCCAAAACATTGCTCCGACCAATCCGCGGCCACCAACTGGGTCCAAACC	312
Db	39784	AACGATCAGCTGGCTCCCTCGCTCCGACCTCCGCGCGCGCGCTTGTCTCAGAAC	39843
Qy	313	AAGTCCAGGCTTACCCAAAAGTTGCCCTTCGATCATCGCGTGGGAAACGAAGTCAATC	372
Db	39844	AACATCCAGGCGTTCCTCCGGCGCTCAACTTCCGCTACATCAGCGTGGCAACGAGG---TT	39900

Qy	373	CCCGCGGCCAAGCTCAGTACGTCTCTCCAGCCATGAACAACATACATAGTCGCGCTCTCC	432
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Qy	433	TTGCGCGGCTTCAGAACATCAAGGTTCACATCATGTCTCTTCGCGGTGCTCGGTACC	492
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Qy	493	TCATATCCCGCTCAGCTGGCTCTCTCTTCCGATGCATCGTGCATTTGGGTCCCAATC	552
Db	40018	GGCTTCCGCGCTCCGCGGCAAGTCTTCCGCC-----TCGCAATGGGGCCCAT	40068
Qy	553	ATACAGTTTCTAGCCAGCAATGGCTCCGCCATTCTTGCCAACTATACCCCTACTTTGAGC	612
Db	40069	GCTCAGTACCTGGGCGACACCGGCGCGCGTGTCTGCGCAACGTCTACCCCTACTTCGCC	40128
Qy	613	TATGCTGGCAACTCCGGATCCATCGACTCTCTATACGCGCTCTTTTACTGCAATCTGGTACA	672
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Qy	673	GTGCTACAGGACGGGTCTTAGCTTACAAACCTCTTCGATGCATGCTCGAGCATGTG	732
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Qy	733	TACTCGGCTTCGAGAGCGCGGAGGCGCGAATCTCCCTGTCTGTCTCGAGAGTGGC	792
Db	40249	TACTCGGCTTCGAGAGCGCGGAGGCGCGGAGCTCCCGATCGTGTCTCGAGAGCGGG	40308
Qy	793	TGGCGCTCAGCGCGGAGCAGCGGCGACGGTGTCTAATGGCGAGCTTACAATCCAAAT	852
Db	40309	TGGCGCTCAGCGCGGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	40368
Qy	853	TTGATCAACCATGTGGGTTCAGGCGCGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGG	912
Db	40369	CTGATCAACCATGTGGGTTCAGGCGCGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGG	40428
Qy	913	TTTGCCATGTTCAACGAGGATCAGAGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	972
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Qy	973	TTTTACCTTACGAAACAGCTGTCTATTCGATCAGCTTCACTTGAGAAATTT	1024
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RESULT 8
AP004031
LOCUS
DEFINITION
PAC clone: P0432C03.
ACCESSION
AP004031 BA000010
VERSION
AP004031.3 GI:18844943
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE	1
AUTHORS	Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T., Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y., Antonio, B. A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K., Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arita, K., Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y., Ito, Y., Idonuma, A., Iijima, M., Ikeda, M., Ikeno, M., Ito, S., Ito, T., Ito, Y., Kikuta, A., Kobayashi, N., Kono, I., Machita, K., Maehara, T., Mizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M., Nakama, Y., Nakamichi, Y., Nakamura, M., Namiki, N., Negishi, M., Onaka, I., Ono, N., Saji, S., Sakai, K., Shibata, M., Shimokawa, T., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., Yamagata, H., Yamane, H., Yoshiki, S., Yoshihara, R., Yukawa, K., Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,


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QY 253 AACTCCGACCTCCAAACATTCCTCCGACCAATCCGCGGCCACCACTGGGTCCAAAC 312
Db 31277 AACGATCAGTCCGCTCCCTCGCTCCGACCCCTCCGCGGCCGCTTCGTCCAGAAC 31336

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RESULT 9

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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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PUBMED
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AUTHORS
TITLE
JOURNAL
FEATURES
source
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222874.1 GI:311763
(1,3; 1,4) beta glucanase.
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Triticum aestivum
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 1426)
Lai,D.M., Hoj,P.B. and Fincher,G.B.
Purification and characterization of (1-->3, 1-->4)-beta-glucan
endohydrolases from germinated wheat (Triticum aestivum)
Plant Mol. Biol. 22 (5), 847-859 (1993)
8358032
2 (bases 1 to 1426)
Fincher,G.B.
Direct Submission
Submitted (01-JUN-1993) Fincher G. B., University of Adelaide,
Waite Campus, Plant Science, Glen Osmond, South Australia,
Australia, 5064

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3' UTR

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Query Match 37.5%; Score 422; DB 15; Length 1426;

Best Local Similarity 64.7%; Pred. No. 2.5e-73;

Matches 661; Conservative 0; Mismatches 355; Indels 6; Gaps 2;

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DEFINITION
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ACCESSION
AF004838
VERSION
AF004838.1 GI:6448756
KEYWORDS
Musa acuminata
SOURCE
Musa acuminata
ORGANISM
Musa acuminata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.
1 (bases 1 to 1041)
Chen, Y.-C., Do, Y.-Y. and Huang, P.-L.
Isolation and nucleotide sequence of a fruit ripening-related cDNA
encoding glucan endo-1,3-beta-glucosidase homolog from banana
(Accession No. AF004838) [PGR97-151]
Plant Physiol. 115 (2), 864 (1997)
2 (bases 1 to 1041)
Huang, P.
Direct Submission
Submitted (20-MAY-1997) Horticulture, National Taiwan University,
No.1 Section 4 Roosevelt Road, Taipei, Taiwan 10617, Republic of
China

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QY 8 GCAGTTCACAAAGAGTGCATCGATTGTGTCTGCTACGGCATGCTCGCAACAATCTT 67
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Best Local Similarity 68.3%; Pred. No. 2.7e-73;
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AK070677

LOCUS

DEFINITION *Oryza sativa* (japonica cultivar-group) cDNA clone. J023063017, full insert sequence.

ACCESSION

AK070677

VERSION

AK070677.1

KEYWORDS

FLI CDNA; CAP trapper.

SOURCE

AK070677*

1295 bp mRNA linear

PLN 24-JUL-2003

Oryza sativa (japonica cultivar-group) cDNA clone. J023063017, full insert sequence.

AK070677

GI:32980701

FLI CDNA; CAP trapper.

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; *Oryza*.

REFERENCE

AUTHORS

1 The Rice Full-length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ohtsuki, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurotsaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nariakawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawaj, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Oza, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.

Japonica rice
Collection, mapping, and annotation of over 28,000 cDNA clones from

Science 301 (5631), 376-379 (2003)

12869764

2 (bases 1 to 1295)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Koda, T., Kojima, K., Kurotsaki, T., Kusumegi, T., Li, C., Lu, M., Koya, S., Kurihara, C., Kurotsaki, T., Matsuyama, T., Miura, J., Miyazaki, A., Masuda, H., Matsubara, K., Matsuyama, T., Mizuno, K., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariakawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Oza, Y., Ohtsuki, R., Saitoh, H., Sasaki, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tegawa, A., Takahashi, P., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toyota, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission

Submitted (05-DSC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice. URL: <http://cdna01.dna.affrc.go.jp/cdna/>

NTAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,

Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ohtsuki, T., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotsaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariakawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,

[illegible]

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Db	1103 T 1103		
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DEFINITION	Oryza sativa beta-1,3-glucanase precursor (Gns5) gene, complete cds.		PLN 27-JUN-2000
ACCESSION	U72251		
VERSION	U72251.1	GI:4097939	
KEYWORDS			
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
REFERENCE	1 (bases 1 to 1834)		
AUTHORS	Romero,G.O., Simmons,C., Yaneshita,M., Doan,M., Thomas,B.R. and Rodriguez,R.L.		
TITLE	Characterization of rice endo-beta-glucanase genes (Gns2-Gns14) defines a new subgroup within the gene family		
JOURNAL	Gene 223 (1-2), 311-320 (1998)		
PUBLISHED	9858757		
REFERENCE	2 (bases 1 to 1834)		
AUTHORS	Romero,G.O., Simmons,C.R. and Rodriguez,R.L.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-SEP-1996) Molecular and Cellular Biology, University of California at Davis, Davis, CA 95616, USA		
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RESULT 14
AY612193 1249 bp mRNA linear PIN 03-MAR-2005
LOCUS Hordeum vulgare beta-1,3-glucanase 2a mRNA, complete cds.
DEFINITION
ACCESSION AY612193
VERSION AY612193.1 GI:51860172
KEYWORDS
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 1249)
Troedson,U., Green,B., Widell,S., Collinge,D. and Bryngelsson,T.
Isolation and characterization of three beta-1,3 glucanases from
barley leaves (Hordeum vulgare, L.) infected by the powdery mildew
fungus Blumeria graminis f. sp. hordei
Unpublished
2 (bases 1 to 1249)
Troedson,U., Green,B., Widell,S., Collinge,D. and Bryngelsson,T.
Direct Submission
TITLE Submitted (29-APR-2004) Cell and Organism Biology, Solvegatan 35B,
Lund 22362, Sweden
FEATURES
Location/Qualifiers
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source

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CDS

ORIGIN

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38	310	27.6	1949	2	AAZ33531	310	27.6	1949	2	AAZ33531	310	27.6	1949	2	AAZ33531
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ALIGNMENTS

RESULT 1
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ID ADY53162 standard; cDNA; 1125 BP.
XX
AC ADY53162;
XX
DT 19-MAY-2005 (first entry)
XX
DE Lily beta-1, 3 glucanase cDNA, LPGLul.
XX
KW Beta-1, 3 glucanase; glucan endo-1, 3 glucan glucanhydrolase;
KW transgenic plant; disease resistance; crop improvement;
KW plant fungal disease; antifungal agent; plant; gene; ss.
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OS Liliaceae.
XX
FH Key Location/Qualifiers
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PF 26-AUG-2003; 2003US-00647649.
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PR 26-AUG-2003; 2003US-00647649.
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PA (CHEN//) CHEN C.
PA (HOU//) HOU P.
XX
PI Chen C, Hou P;
XX
DR WPI; 2005-195288/20.
DR P-PSDB; ADY53161.
XX
PT New nucleic acid sequence encoding beta-1,3-glucanase, useful for
PT producing a transgenic plant with enhanced resistance against fungi.
XX
PS Example 2; SEQ ID NO 2; 14pp; English.
XX

CC The present invention relates to beta-1, 3 glucanase polynucleotide and
CC its encoding polypeptide obtained from lily plant. The invention is
CC useful for producing a transgenic plant with enhanced resistance against
CC a wide variety of stresses particularly fungal attack such as Botrytis
CC blight and gray mold. The polypeptide of the invention is also capable of
CC degrading the cell wall of fungi and thus can be used as an antifungal
CC agent. The present sequence is lily beta-1, 3 glucanase cDNA, LPGA1ul
CC (lily pathogen-induced glucanase 1).
XX
SQ Sequence 1125 BP; 272 A; 356 C; 245 G; 252 T; 0 U; 0 Other;
Query Match 100.0%; Score 1125; DB 14; Length 1125;
Best Local Similarity 100.0%; Pred. No. 9.6e-278;
Matches 1125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TTCTAGGCGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCTTTGTAGTACTC 60
Qy 61 TCGGCATCCCGAGGGGCTGGATCCATTTGGGGTCTGCAATGGATGGACGGTGCACAC 120
Db 61 TCGGCATCCCGAGAGGGCTGGATCCATTTGGGGTCTGCAATGGATGGACGGTGCACAC 120
Qy 121 CTCCCCAGCCCGCGAGCTCGTCAACCTCTACAGTCCAAACAACATAGCTGGCATGCGA 180
Db 121 CTCCCCAGCCCGCGAGCTCGTCAACCTCTACAGTCCAAACAACATAGCTGGCATGCGA 180
Qy 181 CTCTAAGCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACTCATC 240
Db 181 CTCTACAGCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACTCATC 240
Qy 241 CTGACGTCCTCCAACTCGACTCTCAAAACATTGGCTCGACCAATCGCGCGCCACCAAC 300
Db 241 CTGACGTCCTCCAACTCGACTCTCAAAACATTGGCTCGACCAATCGCGCGCCACCAAC 300
Qy 301 TGGGTCCAAACCAAGCTCCAAAGCTTACCCAAAGCTTTCGATACATCGCGTGGGA 360
Db 301 TGGGTCCAAACCAAGCTCCAAAGCTTACCCAAAGCTTTCGATACATCGCGTGGGA 360
Qy 361 AACGAAGTCATCCCGGGCGCCAGCTCAGTACGTCCTCCAGGCCATGAACAAACATACAG 420
Db 361 AACGAAGTCATCCCGGGCGCCAGCTCAGTACGTCCTCCAGGCCATGAACAAACATACAG 420
Qy 421 TCGGCCCTCTCTCTGCGGGCTTCAGAAACATCAAGGTCTCCACATCAGTCTCCTTCGGC 480
Db 421 TCGGCCCTCTCTCTGCGGGCTTCAGAAACATCAAGGTCTCCACATCAGTCTCCTTCGGC 480
Qy 481 GTCGTCGGTACTCATATCCCTCCCTCAGTGGCTCTCTCTCCGATGCATCGTCGACA 540
Db 481 GTCGTCGGTACTCATATCCCTCCCTCAGTGGCTCTCTCTCCGATGCATCGTCGACA 540
Qy 541 TTGGGTCCAAATCATAAGTTTCTAGCCAGCAATGGCTCCCAATTAATTGCCAACATCTAC 600
Db 541 TTGGGTCCAAATCATAAGTTTCTAGCCAGCAATGGCTCCCAATTAATTGCCAACATCTAC 600
Qy 601 CCTACTTTGAGTATGCTGGCACTCCCGATCCATCGACCTCTCATACGCCCTCTTTACT 660
Db 601 CCTACTTTGAGTATGCTGGCACTCCCGATCCATCGACCTCTCATACGCCCTCTTTACT 660
Qy 661 GCATCTGGTACAGTCTGACAGCGGGTCTTACGCTTCAACAACCTCTTCGATGCCATG 720
Db 661 GCATCTGGTACAGTCTGACAGCGGGTCTTACGCTTCAACAACCTCTTCGATGCCATG 720
Qy 721 GTCGACGATTTACTTCGGCCCTTGAGAGCGCGGAGGGCCGAATGTCCTCTTTGTCGTG 780
Db 721 GTCGACGATTTACTTCGGCCCTTGAGAGCGCGGAGGGCCGAATGTCCTCTTTGTCGTG 780
Qy 781 TCGGAGTGTGCTGCGCTCAGCGGGCGGACAGCGGGCGAGCGGTCTTAATGCGCAGACT 840
Db 781 TCGGAGTGTGCTGCGCTCAGCGGGCGGACAGCGGGCGAGCGGTCTTAATGCGCAGACT 840
Qy 841 TACAATTCCAATTTGATCAACCATCTGGGTCAAGGGGAGCGCGGAGGCGCCAGGCGCGGATT 900
Db 841 TACAATTCCAATTTGATCAACCATCTGGGTCAAGGGGAGCGCGGAGGCGCCAGGCGCGGATT 900

Db 841 TACAATTTCCAATTTGATCAACCATCTGGGTCAAGGGGAGCGCGGAGGCGCGGCGATT 900
Qy 901 GAGACCTACATATTTGGCATGTTCAACAGAGATCAGAAGCAGCCGCAAGGATTTGAGAAT 960
Db 901 GAGACCTACATATTTGGCATGTTCAACAGAGATCAGAAGCAGCCGCAAGGATTTGAGAAT 960
Qy 961 AACTTTTGGGCTGTTTACCCCTTAACGACAGCTCTCTATTTCGATCAGCTTCACCTTGAGAA 1020
Db 961 AACTTTTGGGCTGTTTACCCCTTAACGACAGCTCTCTATTTCGATCAGCTTCACCTTGAGAA 1020
Qy 1021 ATTTGATCAGATGAATATAATAAAGAGTCTTATATTGTAAGGCAAGCTCGTAATTGA 1080
Db 1021 ATTTGATCAGATGAATATAATAAAGGCTTATATTGTAAGGCAAGCTCGTAATTGA 1080
Qy 1081 TAGCCATCTAGTATATAGCTCCGGCTAAATTAACCTATATAAATA 1125
Db 1081 TAGCCATCTAGTATATAGCTCCGGCTAAATTAACCTATATAAATA 1125
RESULT 2
ADA69575
ID ADA69575 standard; DNA; 993 BP.
XX
AC ADA69575;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 2898.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
XX
KW gene; ds.
XX
OS Oryza sativa.
XX
FN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 2898; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 993 BP; 190 A; 356 C; 285 G; 162 T; 0 U; 0 Other;
Query Match 38.3%; Score 431.2; DB 8; Length 993;
Best Local Similarity 67.2%; Pred. No. 4.9e-100;
Matches 677; Conservative 0; Mismatches 313; Indels 18; Gaps 4;


```
QY 241 CTCGACGTCCTCCCACTCCGACCTCCAAACATTGGCTCCGACCAATCGCGCGCCACCAAC 300
Db 265 TTGGATGTCCCAAACTACTCGTCTCAATCATTTGGCTCTAGCCCTTCAGCAGCTAAACAAT 324
QY 301 TGGGTCCAAACCAACGTCCTCAAGCCTA---CCAAACGTTGGCTTCGATACATCGCGTC 357
Db 325 TGGGTCCAGCAAAATGTGAAGCCTATTCTTCTGGTGTTTCATTAAATACATCGAGTT 384
QY 358 GGAACGAAGTCAATCCCGCGGCGCAAGCTCAGTACGTCCTCCAGCGCATGAACAACATA 417
Db 385 GGAATGAAGTGAATTCCTGGAGCTGAAGCCCAATATGTCTCCCTGCCATGAGAAACATC 444
QY 418 CAGTCGCGCTCTCTCTGCGCGGCTTCAGAAC---ATCAAGGTCTCCACATCAGTCTCC 474
Db 445 TATTCAAGCTCTTCTCTCGCTGGGCTACAAACCAAAATAAAAGTCTCAACTGCACTCGCC 504
QY 475 TTCGGGTCGTCGGTACCTCATATATCCCTCCCTCAGCTGGCTCTCTCTTCGGATGCAATCG 534
Db 505 ACTTCAGTCTCTGGGAATCAATTTCTCTCCCTCAACAGGGGCAATCTCTCTGCTGCAATG 564
QY 535 TCGACATTTGGGTCCAAATCATACAGTTTCTAGCCAGCAATGGCTCCCAATTAATTTGCCAAC 594
Db 565 ACATATTTGAGTCCCAATAGTTCAATTTTGGTGTAGTAATGAGCACCACCTCTGTGTAAT 624
QY 654 ATCTACCCCTACTTGAGCTATGCTGGCACTCCGGATCCATCGACCTCTCATACGCCCTC 654
Db 625 GTATACCCCTACTTTCAGTTATGTGAATATGTAATACCGAACCAAAATCAACATTTGAATATG 684
QY 655 TTTACTGATCTGGTACAGTCTGATACAGGAGCGGCTCTACGCTTACAAACAACTCTTCGAT 714
Db 685 TTTACTTCCCGGAGCTGTAGTGACAGATGACATTAATAATTCAGAACCTCTTTGAT 744
QY 715 GCCATGTCGACGCAATTTACTTCGGCCCTCGAGAGCGCCGAGGCGCGGAATGTCCCTGTT 774
Db 745 GCCATGTTGATGCAATTTATGCGGCAATTCGAGAAGTTCGAGAGGCTTAATGTGGCGATA 804
QY 775 GTGCTGTCGAGAGTGGCTGGCCGCTCAGCGGGCGGAGCGGAGCGGTGTCTAATGCG 834
Db 805 GTGCTGTCGAGAGCGGTTGGCCATCAGCTGGTGTACTGCGAGCAACCATCAACAAATGCA 864
QY 835 CAGACTTACAATTCAAATTTGATCAACCATGTTGGTTCAGGGGAGCGCGGAGGCGCAGG- 893
Db 865 AAGACATATATCAGAAATTTGATCAATCATGTTGTTCAAGGACTCCAGAGATCTGGA 924
QY 894 --GGCGATGAGACTACATATTTGCCATGTTCAACGAGGATCAGAGCAGCCGCAAGGG 951
Db 925 AAGGCTATAGAGGCTTACATATTCGAGATGTTCAATGAGATTTGAAATCATCG--GGA 981
QY 952 ATTGAGATTAATTTGGGCTGTTTACCTTAACGAAACAGCTGTCTATTGATCAGCTTC 1011
Db 982 ATTGAACAAAATTTGGACTGTTTACCCAAATATGCAACCAAGTCTACCCAATCAACTTT 1041
QY 1012 ACTTGAGAAATTTGATCAGATGAATAATAATAA 1045
Db 1042 ACTTGAATGCCAGAGCGCCATATATAATAGTAA 1075
```

RESULT 4

ADT19801

ID ADT19801 standard; cDNA, 1439 BP.

XX AC

ADT19801;

XX AC

13-JAN-2005 (first entry)

XX DT

Plant cDNA, Seq ID 5127.

XX DE

XX Plant; ss; gene; transgenic; cold tolerance; growth rate;
KW drought tolerance; disease resistance; galactomannan production;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW lignin production; extreme osmotic condition tolerance;
KW pathogens resistance; pest resistance; yield improvement; seed oil yield;

seed protein yield.

Viridiplantae.

US2004216190-A1.

28-OCT-2004.

18-DEC-2003; 2003US-00739930.

28-APR-2003; 2003US-00424599.

28-APR-2003; 2003US-00425115.

(KOVA/) KOVALIC D K.

Kovalic DK;

WPI; 2004-757369/74.

New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.

Claim 1; SEQ ID NO 5127; 14pp; English.

The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for nitrogen use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant cDNA sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20040216190.

Sequence 1439 BP; 308 A; 472 C; 398 G; 259 T; 0 U; 2 Other;

Query Match 38.0%; Score 427.2; DB 13; Length 1439;

Best Local Similarity 66.0%; Pred. No. 5.9e-99;

Matches 656; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 21 CATCTCCATGCTGCCATGCGATCCCTCTTGTAGTACTCTCGCAATCCGAGAGCGGT 80

Db 96 CATGTTTGGGTGGCGTGGCCCTCTCTGGAGTGTCTTGGGATCCATCTCTCGACGCGT 155

2798 GAGCGGGTGGCGTGGCGGGCGGAGGAGCCGAGGAGCAGCAGCAACGCGCAGACGTA 2857
 843 CAAATCCAAATTTGATCAACCATGTGGTTCAGGGAGCGCGAGAGCCAGG---GGCAT 899
 2858 CAACGAGAACTTGATCAGCATGTGGCGGAGGAAACGCGGAGGAGCAGGGAAGGAGAT 2917
 900 TGAGACCTTACATATTTGCGCATGTTCAACGAGGATCAGAGCAGCGCAAGGATTTGAGAA 959
 2918 CGAGCATACATATTCGAGATGTTCAACGAGNACGAGA---AGGCTGAGGATCGAGCA 2974
 960 TAACTTTGGCGTGGTTTACCTTAACGAAACAGCTCTCTATTGATCAGCTTCACTTGAGA 1019
 2975 GAACTTTGGCGTGGTTTATCCCAACGAGCAGCGCGTATACCAATAAGCTTTTAAACT 3034
 1020 AATTTGATCAGATGAATATAA 1041
 3035 AACTTTGTAAGGTTGATGAATCA 3056

RESULT 8
 AAX33557
 ID AAX33557 standard; DNA; 912 BP.
 XX AC
 XX AAX33557;
 XX 07-JUL-1999 (first entry)
 XX DE Rice beta-glucanase Gns5 encoding DNA.
 XX KW Rice; beta-glucanase; Gns; promoter; plant resistance; expression;
 KW fungal infection; transgenic monocotyledon; growth; ss.
 XX OS Oryza sativa.
 XX PN WO9859046-A1.
 XX PD 30-DEC-1998.
 XX PF 25-JUN-1998; 98WO-US013525.
 XX PR 25-JUN-1997; 97US-0050675P.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Rodriguez RL;
 XX DR WPI; 1999-105620/09.
 XX DR P-PSDB; AAY09294.
 XX PT New polynucleotides which hybridise with rice beta-glucanase genes -
 PT useful for transforming monocot plants for various characteristics
 PT including increased resistance to fungal infection.
 XX PS Claim 4; Page 48-49; 90pp; English.

The present invention describes isolated polynucleotides (PN) comprising a sequence which hybridises under high stringency with a rice beta-glucanase gene. Also described are: (A) a chimeric gene (CGI) used to produce a transgenic monocot plant, comprising: (i) a transcriptional regulatory region which hybridises under high stringency with a rice beta-glucanase promoter; and (ii) a DNA sequence heterologous to the regulatory region, and encoding a protein to be produced by the plant; and (iii) a second DNA sequence encoding a signal polypeptide operatively linked 5' to 3', so that the signal polypeptide is in translation frame with the protein, and is effective to facilitate secretion of the protein across aleurone or scutellar epithelium layers into the endosperm of seeds obtained from the plant; (B) a monocot plant stably transformed with CGI; (C) seeds from the above plant; (D) a method of enhancing the resistance of a monocot plant to fungal infection by stably transforming it with CGI; (E) a method of producing a heterologous protein, comprising stably transforming a plant with CGI, obtaining seeds from the transformed plant, germinating the seeds and obtaining the protein from the seed endosperm; (F) an isolated protein having the characteristics of

CC a rice beta-glucanase enzyme, corresponding to beta-glucanases 2-9 (Gns 2-9). The polynucleotides of the invention are useful to transform monocot plants. The polynucleotides and the proteins produced may also provide increased resistance to fungal infection, improved growth characteristics, and high expression levels of heterologous proteins in various tissues obtained from the plant
 XX
 SQ Sequence 912 BP; 174 A; 326 C; 275 G; 137 T; 0 U; 0 Other;
 Query Match 36.6%; Score 411.2; DB 2; Length 912;
 Best Local Similarity 67.0%; Pred. No. 6.3e-95;
 Matches 619; Conservative 0; Mismatches 293; Indels 12; Gaps 2;
 QY 88 ATTGGGCTCGCAATGGAATGGAGTGGACACCTCCCGAGCGCGCGTGGTCAAC 147
 DB 1 ATCGGCGTGTCTACGGCGTATCGGGAACAACTCGCGTGGAGGAGCGTGGTGCAG 60
 QY 148 CTCTACAAAGTCCAAACACATAGCTGGCATGCGACTCTACAGCCCGCAGCAAGCCACTCTC 207
 DB 61 CTCTACAAAGTCCAAAGCGCATCGACTCCATGGCATCTACTTCCCAAGAGGAGCATCTCTC 120
 QY 208 CAGGCGCTCCAGGGCTTAACTAATCTATCTCTGACGTCCTCCAACTCCGACCTCCAA 267
 DB 121 CAGGCGCTCAGCGGCTCAAGCATGCGCTCACCATGGACGTGGCAACGATCAGTCTGCGC 180
 QY 268 AACATTGCTCCGACCAATCCGCGCCACCACTGGGTGCCAAACCAAGCTCCAGCCTTAC 327
 DB 181 TCCCTCGCCTCCGACCCCTCCGCGCGCGCCCTTCGTCGAGAACAACTCAGCGCTTC 240
 QY 328 CCAAAAGCTGTGCTTCCGATATCATCGCGTCCGGAACGAAGTCAATCCCGCGCGGCCAAGCT 387
 DB 241 CCGGCGTCAACTTCGCTACATCACTGCGCAACGAGG---TTTCGGCGGGGACAG 297
 QY 388 CAGTACGTCCTCCAGCCATGAAACAAATACAGTCCGCGCTCTCTCTGCGCGCTTCAG 447
 DB 298 CAGAACATCTCTCCGCGCATGCAGAACATGAACAGGGGCTCTCGCGCGCGGGCTCGGG 357
 QY 448 AACATCAGGTCCTCCATCATGCTCTCTCGCGCTGCTGGTACCTCATATCCCGCTCA 507
 DB 358 AACATCAGGTCCTGAGTCTGCTGCGCGGAGGTTGGCAACGCGCTTCCCGCGCTCC 417
 QY 508 GCTGCTCTCTCTCTCGATGATCGTGCAGATTTGGGTCCAAATCATACAGTTCCTAGCC 567
 DB 418 GCGGGAGGTTCTCGCC-----TCGACATGGGGCCCATAGTTCAGTCTAGTGGG 468
 QY 568 AGCAATGCTCTCCCATTTGCGCAACATCTACCCCTACTTTGAGCTATGCTGGCAACTCC 627
 DB 469 AGCACCGGGGGCGGCTGCTCGCAACGCTCTACCCCTACTTTCGCTAGCTGCGCAACAGG 528
 QY 628 GGATCCATCGACCTCTCATACGCGCTCTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 687
 DB 529 GCCCAGATCGACATCAACTAGCGCTCTTTCAGCTCGCGCGGAGCGGTTGGTGGAGGACGCG 588
 QY 688 TCCTACGCTTACAAACAACTCTTCGATGCCATGCTGCAGCATTTGTATCTCGCGCTCGAG 747
 DB 589 GGCAACGGTTACAGAACCTGTTTCGACGCAATCGTGCAGACGTTCTACTCTCGCGCTGAG 648
 QY 748 AGCGCGGAGGGCGAATGTCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
 DB 649 AGCGCGGCGCGGAGGCGTCCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
 QY 808 GGGACAGCGGCGAGCGGTGCTTAATGCGCAGACTTACATTTCCATTTGATCAACCATCTG 867
 DB 709 GGCAACGGCGCGGCGCGGCAACGCGCAGACGTCACAAACCAAGAACCTGTATCAACCGCTC 768
 QY 868 GGTGAGGGGAGCGCGAAGAGGCGGAGGCGGATTCAGACCTACATATTTGCCATGTTCAAC 927
 DB 769 GGGCAGGGGAGCGCGCAGAGGCGCGGAGCATTCAGACCTACATTTTCGCCATGTTCAAC 828
 QY 928 GAGGATCAGAGAGCGCGCAAGGGATGAGAAATACTTTGGGCTGTTTAACTTCAACGAA 987
 DB 829 GAGAACAGAGGAGGCGGAGCAGCAGCAGCGGAGGAGCACTTCGCGCTCTTTCACACCGGACGAG 888

QY 988 CAGCGTGTCTATTCGATCAGCTTC 1011
 Db 889 TCGCGGCATCTCTCCATCAATTC 912

RESULT 9

AAQ24291
 ID AAQ24291 standard; DNA; 1463 BP.

AC AAQ24291;

XX 02-NOV-1992 (first entry)

XX (1-3,1-4)-beta-glucanase isoenzyme EI (2).

XX Distal promoter; EI; beta-glucan; endosperm; beer production; ss.

XX Hordeum vulgare.

XX Key Location/Qualifiers
 CDS 68..1072

FT /*tag= a

FT /label= EI

FT 68..151

FT /*tag= b

FT 152..1069

FT /*tag= c

FT 1410..1414

FT /*tag= d

XX WO9205258-A.

XX 02-APR-1992.

XX 20-SEP-1990; 90AU-00002401.

XX 20-SEP-1990; 90AU-00002401.

XX (UYLT-) LA TROBE UNIV.

XX Fincher G;

XX WPI; 1992-150484/18.

DR P-PSDB; AAR23602.

XX DNA encoding barley (1-3,1-4)-beta-glucanase isoenzyme(s) EI and EI1 -
 used to improve quality of barley for malting and brewing processes.
 PS Disclosure; Fig 9; 75pp; English.

XX This sequence encodes the 1463bp cDNA of barley (1-3,1-4)-beta-glucanase
 isoenzyme EI. This sequence is derived from a transcript from the distal
 promoter of the (1-3,1-4)-beta-glucanase isoenzyme EI gene. (See also
 AAQ24290.) EI is synthesized in germinating barley grain where it acts to
 depolymerise the beta-glucans in the cell walls of the starchy endosperm.
 Low levels of the enzyme leads to high levels of the glucans and this can
 cause a reduced malt quality, serious filtration difficulties in the
 brewing process and can contribute to haze formation in the final
 product. The isolated EI gene can be transferred to plants to generate
 varieties which have improved malting and brewing properties.
 CC Alternatively the gene can be introduced into yeast to remove residual
 CC beta-glucan in beer prodn. This protein can be mutated to generate a more
 CC thermostable enzyme

XX Sequence 1463 BP; 303 A; 468 C; 421 G; 271 T; 0 U; 0 Other;

Query Match 36.3%; Score 408.6; DB 2; Length 1463;

Best Local Similarity 64.0%; Pred. No. 3.5e-94;

Matches 650; Conservative 0; Mismatches 359; Indels 6; Gaps 2;

QY 4 ATGGCAGTCTCAGCAGCATCTCCATGCTGCGATGCGATCCCTCTGTAGTACTCTCG 63

Db 68 ATGGCAGGCCAAGGCGTTGCTCTCCATGTTGGCTCTGGCATTTGCTCTCGAGCCTTCGCC 127

QY 64 GCAATCCCGAGAGGCGTGGAAATCCATTTGGGGTCTCAATGGAAATGGAGGTGACAACTTC 123
 Db 128 TCCATCCCAACAAGCGTGGAGTCCATCGGGGTGTCTACGGCATGAGCGCAACAATCTG 187
 QY 124 CCCAGCGCGCGAGCGTCTACCTCTCAAGTCCAAACAATAGCTAGCTGGCATGGACTC 183
 Db 188 CCGCGCGGAGCACCCTGTCTCAAGTCTCAAGTCCAAACGGGATCAACTCTCCATCGGGTG 247
 QY 184 TACAGCCCCGACCAAGCCACTCTCCAGGCGCTCCAGGGCTCTAAACATCTACCTCATCTC 243
 Db 248 TAGCTCTCCGACAGCGCGCTGACGGGTGGCGGACGGGCGTGAACGTTGTGTG 307
 QY 244 GACGTCCCAACTCCGACCTCCAAACAATTGCCTCCGACCAATCCCGCGCCCAACAACCTGG 303
 Db 308 GCGCGCCCAACGACGTCTCTCCAACTCCGCGCAGTCCCGCAGCGCTGCATCGTGG 367
 QY 304 GTCCAAACAAGCTCCAGCTTACCCAAAGCTTGGCTTCGGATACATCGCGCTCGGAAC 363
 Db 368 GTGAGGAGCAACATCCAGGCGTACCCCAAGGTCTCTTCGGTACGTCTCGCTGGGCAAC 427
 QY 364 GAAGTCATCCCGCGCGCAAGCTCAGTACGTCTCCAGGCGCATGAAACAATACAGTCC 423
 Db 428 GAGG---TCCCGCGCGCGCCACCAGAACTTGTCCCGCGCATGAAGACGTGCGGGC 484
 QY 424 GCGCTCTCTCTGCGCGCTTTCAGAAATCAAGGTCTCCACATCAGTCTCTTTCGGCGTC 483
 Db 485 GCGTGGCTCTCGCGCGCTGGGCGCCACATCAAGGTGACCAAGTCTCGCAGCGCATC 544
 QY 484 TCGGTACCTCATATCCCGCTTCAGTGGCTCTCTTCCTTCGATGATCTGTCGATG 543
 Db 545 CTGGGGGTGTACAGCCCGCGCTCCCGCGGTCTTACCGGAGAGCGGCGTTCATG 604
 QY 544 GGTCCAAATCATACAGTTTCTAGCCAGCAATGGCTCCCAATTAATGCGCAATCTACCCC 603
 Db 605 GCGCGCGGTGTGAGTCTCTTGGCGCGCACCGCGCGCGCTCATGGCCAAATCTACCCG 664
 QY 604 TACTTGAGCTATGCTGCAACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACTGCA 663
 Db 665 TACCTGGCTGGGCTTACNACCCGAGCGCATGACATGAGCTAGCGCTCTTCAACCGC 724
 QY 664 TCTGTACAGTCTGACAGGCGGTCTTACGCTTACAAACAACCTCTTCGATGCCATGTC 723
 Db 725 TCCGCAACCGTGTCTCAGGACGGCTCTTACGGGTACCAAGAACCTGTTTCGACACACCGTG 784
 QY 724 GACCATTTGTTACTCGGCTTGGAGAGCGCCCGAGGGCGCAATGTCCTGTTGTCTGTCTG 783
 Db 785 GACGCTTCTTACACGGCGCATGGCCAAAGCACACGGCGGCTCCAAACGTGAAGCTGGTGTGTC 844
 QY 784 GAGAGTGGCTGGCGCTCAGCGGGCGGACAGCGCGAGCGGTGTCTAATGCGCAGACTTAC 843
 Db 845 GAGAGCGGTGGCGCTCAGCGCGGCGACGCGCGGCGACCCCGCGCCAGGATCTTAC 904
 QY 844 AATTCCAATTTGATCAACCACTGTGGGTGAGGGGACGCGGAGAGAGAGAGAGAGAGAGAG 903
 Db 905 AACCAGTACCTCATCAACCACTGTGGGTGAGGGGACCCCGCGCGCGCGCGCGCGCGAG 964
 QY 904 ACCTACATATTTGCGATGTTCAAGGAGATCAGAGCGCGCGCGAGGATTTGAGATTAAC 963
 Db 965 ACCTACGCTTCTCTCATGTTTCAACGAGAACCAAGAGGA---CAACGGCGGTGGAGCAGAAC 1021
 QY 964 TTTGGGCTGTTTACCCTTACGAGACGCTCTCTATTTCGATCAGCTTCACTTGG 1018
 Db 1022 TGGGGGCTCTTCTTACCCCAACATGACGACGCTCTACCCCATCTGATGAG 1076

RESULT 10

ADT19681

ID ADT19681 standard; cDNA; 1458 BP.

XX ADT19681;

XX ADT19681;

DT 13-JAN-2005 (first entry)

Plant cDNA, Seq ID 5007.

Plant; ss; gene; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed protein yield.

Viridiplantae.

US2004216190-A1.

28-OCT-2004.

18-DEC-2003; 2003US-00739930.

28-APR-2003; 2003US-00424599.

28-APR-2003; 2003US-00425115.

(KOVA/) KOVALIC D K.

Kovalic DK;

WPI; 2004-757369/74.

New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.

Claim 1; SEQ ID NO 5007; 14pp; English.

The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant cDNA sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in seqdata.uspto.gov/sequence.html?DocID=20040216190.

Sequence 1458 bp; 310 A; 436 C; 417 G; 295 T; 0 U; 0 Other;

		Query Match	35.0%; Score 394.2; DB 13; Length 1458;
		Best Local Similarity 64.9%; Pred. No. 1.7e-50;	
		Matches 617; Conservative 0; Mismatches 328; Indels 6; Gaps 2;	
Qy	75	AGGCGTGGAAATCCAAATGGGGTCTGCAATGGAATGGACGGTCAACACCTCCCCAGCCCGC	134
Db	108	AGGCGTGGAGTCCAAATGGGGTGTGCTACGGCATGAGGCCCAACACTCGCGGGGGGAG	167
Qy	135	CGAGCTGTCAACCTCTTCAAGTCCAAACAACTAGCTGGCATCGACTCTCTACAGCCCCGA	194
Db	168	CACGCTGTGAGCATGTTCAAGTCCAAAGGGTATCAACTCATCGGCTATATGCCCCGA	227
Qy	195	CAAAGCCACTCTCGAGGCCCTCAGGGCTCTAACTACTTACTCTCATCTCGACGTCCCAA	254
Db	228	CCAAGGCGCGCTCGAGGCCGTGCGCGGTACGGGCGTCAACGTCGTCTGTCGGGGCGCTAA	287
Qy	255	CTCGACCTCCAAAACATTTCCCTCCGACCAATCCGGCGCCACCAACTGGGTCCAAAACCAA	314
Db	288	CGAGTGTCTCTCAAACCTTCGCGCGCAGCCCGGCGGCGCGCTCTGTGGTTCAGGAGCAA	347
Qy	315	CGTCCAAAGCTTACCCAAAAGTTGCTTCCGATACATCGCGCTCGGAAACGAAGTCAATCC	374
Db	348	CATCCAGGCTTACCCGGAAGTTTCTTTTCGGTACGCTCTGCGTCCGCAACGAGG---TCGC	404
Qy	375	CGGCGGCCAAGCTCAGTACGTCCTCCAGCCATGAACAACTACATACGTCGCGCTCTCTCT	434
Db	405	CGGCGGTGCCACCAAGAACCTCTGTCGGCCATGAAAAAGCTGACGGGCGCTCGCCTC	464
Qy	435	TGCGCGGCTTCAGAAACATCAAGGCTCTCCACATCAGTCTCTCTCGCGGTGTGTCGTACCTC	494
Db	465	CGCTGGGCTGGGCCACATCAAGGTCACCACTGCTGCTGTCGAGGCCATCTCTCGCGTGTA	524
Qy	495	ATATCCCGCTCAGCTGGCTCTCTTCTTCGATGACATCGTTCGACATTTGGGTCCAATCAT	554
Db	525	CAGCGCGCTCTCGCGGGTCTCTTTCACCGGGAGGGGACGCGCTTCTATGGGCCCCGTGT	584
Qy	555	ACAGTTCTTAGCAGCAATGGCTCCCATTTACTTTCGCAACATCTACCCCTACTTTGAGCTA	614
Db	585	GCAGTCTCTTGGCCGCACCGCGCGCGCTCATTGGCCAACTATCCCGTACTGGCTG	644
Qy	615	TGCTGGCAATCTCGGATTCATCGACCTCTCATACGCCCTCTTTTACTGCTCTGGTACAGT	674
Db	645	GGCTTACAAACCGAGCGCATGACATGAGTACGGCTCTTTCACCGGTCTCGGCAACGT	704
Qy	675	CGTACAGGACGGTCTTACGCTTACAAACACTCTTTCGATGCCATGGTCGACCGCATTTGA	734
Db	705	GGTCCAGGACGGCTCTTACGGGTACCAAGACCTGTTTCGACACCAACCGTGGACGCTTCTA	764
Qy	735	CTCGGCTCTGAGAGCGCGGAGGGCGGAATGTCCTGTTGTCGTTCGAGAGTGGCTG	794
Db	765	CACGGCCATGGCCAAAGCACGGCGCTTCAAAGTGAAGCTCTGTGTCGAGAGCGGGTG	824
Qy	795	GCGCTCAGCGGGGGACAGCGCGACGGTGTCTAATGCGCAGACTTACAATTTCCAATTT	854
Db	825	GCCCTCAGGCGCGGACAGCGCGCGACTCCGGGCCAACGCCCGGATCTTACAACAGTACCT	884
Qy	855	GATCAACCATGTGGGTACAGGGACGCGGAGAGGCCACAGGGCGGATTTGAGACCTTACATTT	914
Db	885	CATCAACCATGTGGGTACAGGGACGCGGAGAGGCCACAGGGCGGATTTGAGACCTTACGTC	944
Qy	915	TGCCATGTTCAAAGGATCAGAAAGCAGCGCAAGGATTTGAAATAACTTTTGGGCTGTT	974
Db	945	CTCAATGTTCAAAGGATCAGAAAGCAGCGCAAGGATTTGAAATAACTTTTGGGCTGTT	1001
Qy	975	TTACCTTAACGACAGCGCTGTCTATTTCGATCAGCTTCACTTTGAGAAATTTG	1025
Db	1002	CTACCCCAACATGACGACGCTCTACCCCATCAGCTTCTGATGAGCTAGCTG	1052

RESULT 11

AAQ24292

ID AAQ24292 standard; DNA; 1257 BP.

XX

AAQ24292;
 02-NOV-1992 (first entry)
 (1-3,1-4)-beta-glucanase isoenzyme EII.
 Distal promoter; EII; beta-glucan; endosperm; beer production; ss.
 Hordeum vulgare.
 Key Location/Qualifiers
 CDS 66..1070
 /*tag= a
 /label= EII
 sig_peptide 66..149
 /*tag= b
 mat_peptide 150..1067
 /*tag= c
 polyA_signal 1210..1214
 /*tag= d
 WO9205258-A.
 02-APR-1992.
 20-SEP-1990; 90AU-00002401.
 20-SEP-1990; 90AU-00002401.
 (UYLT-) LA TROBE UNIV.
 Fincher G;
 WPI; 1992-150484/18.
 P-PSDB; AAR23603.
 DNA encoding barley (1-3,1-4)-beta-glucanase isoenzyme(s) E1 and E11 -
 used to improve quality of barley for malting and brewing processes.
 Disclosure; Fig 10; 75pp; English.
 This sequence encodes the 1229bp cDNA of barley (1-3,1-4)-beta-glucanase
 isoenzyme EII. EII is synthesized in germinating barley grain where it
 acts to depolymerize the beta-glucans in the cell walls of the starch
 endosperm. Low levels of the enzyme leads to high levels of the glucans
 and this can cause a reduced malt quality, serious filtration
 difficulties in the brewing process and can contribute to haze formation
 in the final product. The isolated EII gene can be transferred to plants
 to generate varieties which have improved malting and brewing properties.
 Alternatively the gene can be introduced into yeast to remove residual
 beta-glucan in beer prodn. This protein can be mutated to generate a more
 thermostable enzyme
 Sequence 1257 BP; 261 A; 415 C; 358 G; 223 T; 0 U; 0 Other;

Query Match 35.0%; Score 393.6; DB 2; Length 1257;
 Best Local Similarity 63.3%; Pred. No. 2.3e-90;
 Matches 638; Conservative 0; Mismatches 364; Indels 6; Gaps 2;
 4 ATGGCAGCTCAGCAGCATCTCCATGCTGCGATGCGCATCCCTCTTGTAGTACTCTCG 63
 66 ATGGCGAGCCCAAGGGTTGGCTCCATGTTCACTCTCGCATGCTTCTCGAGCCTTCGCG 125
 64 GCATCTCCGAGAGGGCTGGAATCCATGCTGCGGTCTGCAATGGAATGAGCGTGCACACTC 123
 126 TCTATCCCAACAGCGTGGATGCGATGCGGGTGTCTACGGCATGAGCGCCCAACACTG 185
 124 CCCAGCCCGCGAGCTGCTCAACCTCTACAGTCCAAACATAGCTGGCATGCGACTC 183
 186 CCGGCGGAGCACCCTGTGTGAGCATGTTCAAGTCCAGCGGATCAATCATGCGGCTG 245
 184 TACAGCCCGGAGCAGCATCTCTCAGGCCCTCCAGGCTCTTAACATCTACTCATCTC 243

Db 246 TACGCTCCCAACAGCGCGCGCTGCGGCGCAGCGGCATCAACGCTCGTCGTC 305
 QY 244 GACGTCCTCCCAACTCCGACCTCCAAACATTTGCTCCGACCAATCCGCGCCCACTACGTCG 303
 Db 306 GGGGCTCTTAACGAGCTCTCTCCAACTCCGCGCCAGCCCGGAGCGCGCTCGTG 365
 QY 304 GTCCAAACCAACGCTCCAAAGCCTTACCACAAAGTTGCTTCCGATACATCCCGCTCGGAAC 363
 Db 366 GTCAAGAGCAACATCCAGCGGTACCCCAAGGTTTCTCTCCGCTAGCTCTCGCTCGGAAC 425
 QY 364 GAAGTCATCCCGCGCGCGCAAGCTCAGTACGTCCTCCAGCATTGAACAAATACAGTCC 423
 Db 426 GAGG---TCGCGCGCGCGGCCACCCCGGAACCTCTGCTCCGCGCAATGAAGACGTCATGCG 482
 QY 424 GCCCTCTCTCTGCGCGGCTTCAGAAACATCAAGGTCTCCACATCAGTCTCTCTCCGCGTC 483
 Db 483 GCGCTCGTGGCGCTGGGTGGGCCACATCAAGGTGACCACTCGGTGTGGAGGCGATC 542
 QY 484 GTCGTACTCATATATCCCGCTCAGTGGCTCTCTCTTCGATGCAATCGTCGACATTTG 543
 Db 543 CTGGCTCTGTTACGCGCGCTCCCGCGCTCTTACCGGGAGCGCGCGCTTCATG 602
 QY 544 GGTCCATCATACAGTTTCTAGCAGCAATGGCTCCCAATTAATCTTGCACATCTACCC 603
 Db 603 GGGCGCGGTGGTCCAGGCTTCTTCCCGCACCAACGCGCGCTCATGGCCAACTTTACCG 662
 QY 604 TACTTGAGCTATGCTGGCAACTCCCGATCCCACTCTCATACGCTCTCTTACTGCA 663
 Db 663 TACCTGGCTTGGCTTACACCGGCGCATGGCATGGGTCTCGCTCTCTTCAACGG 722
 QY 664 TCTGTACAGTGTACAGGAGCGGTCTTACGTTTACAAACACTCTTTCGATGCCATGTC 723
 Db 723 TCGGCACCGTGGTTCAGGAGCGGCGCTTACGGGTACAGAACCTCTTTCGACACCCGCTG 782
 QY 724 GACGATTTGACTCGGCGCTCGAGAGCGCGCGGAGCGCGGCGCAATGTCCTTGTGTGTCG 783
 Db 783 GACGCTTCTACAGCGCTATGGGCAACCAACGCGCGCTCAGCGTGAAGCTGGTGTGTCG 842
 QY 784 GAGAGTGGCTGCGCTCAGCGCGGGGACAGCGGCGGCTCTTAATGCGCGACTTAC 843
 Db 843 GAGAGCGGTGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 902
 QY 844 AATTCATTTTGAATCAACCATGTTGGTTCAGGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 903
 Db 903 AACCAGCACTCATCAACCATGTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 962
 QY 904 ACCTACATTTTGCATGTTTCAAGAGATCAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 963
 Db 963 ACCTACATCTTTCGCGCATGTTTCAAGAGAAACGCGGAGGA---CAGCGCGGTGGAGCAGA 1019
 QY 964 TTTGGGCTGTTTACCTTAACGACGCTCTCTATTTCGATCAGCTTC 1011
 Db 1020 TGGGACTCTTTTACCTTAACGACGCTCTCTATTTCGATCAGCTTC 1067

RESULT 12
 ADX51668
 ID ADX51668 standard; cDNA; 1268 BP.
 XX
 AC ADX51668;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polynucleotide seqid 26408.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.

XX Unidentified.
OS US2004034888-A1.
PN 19-FEB-2004.
XX
XX
XX 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.
PA (CAO/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 26408; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1268 BP; 276 A; 439 C; 336 G; 217 T; 0 U; 0 Other;

Query Match 33.9%; Score 381.6; DB 13; Length 1268;
Best Local Similarity 62.9%; Pred. No. 2.7e-87;
Matches 629; Conservative 0; Mismatches 359; Indels 12; Gaps 2;
QY 18 CATCATCTCCATGGCTGCGATGGCATCCCTCTGTAGTACTCTCGGCAATCCCGAGAGG 77
DB 87 CGTCCGCTTCCATGCGATGGCTGGCATCTGCTCGGAGCATTCGAGCCATCTCTACAGG 146
QY 78 CQTGGAATCCATTTGGGGTCTGCAATGGAATGAGCGGTGACCACTCCCGCCAGCCGCGGA 137
DB 147 AGTCATATCCATCGCGGTGTGACGGGTGAGCGGAGCAACCTGCCCCCGGAGGCGA 206
QY 138 CGTCGTCAACCTCTACAAGTCAACAACATAGCTGGCATGCGATCTTACAGCCCGCCGCA 197
DB 207 CGTGGTGCAGCTGTACCAAGTCCACGGCATCAACCTGATGGCATCTACTTCCCGGACGC 266
QY 198 AGCCACTCTCCAGGCCCTCCAGGCTCTAACTATCTACCTATCTCGAGCTCCCACTC 257
DB 267 CAACGCGTGAACGCGCTGAGCGGACCAGCATCGGGCTCATCTATGGAGCTGCCCAACAC 326
QY 258 CGACCTCCAAACATTTGCTCCGACCAATCCCGCCGCCCACTGGGTCCCAACCAAGCT 317

DB 327 GGACCTGCGCTCGCTGGCTCCGAGCCCGAGCGCGCGCGCTTGGGTGAGAGCAACGT 386
QY 318 CCAAGCCTACCCAAACGTTGCTTCCGATACATCGCGTTCGGAACGAGTCAATCCCGG 377
DB 387 GCAGCGGTTCCTCGGTGAGCTTCGCTACATCGCGTGGGCAACGAGG---CCTCCGG 443
QY 378 CGGCAAGCTCAGTACGTCTCCGAGCCATCAACAAATACATAGTCCGCGCTCTCTCTGCG 437
DB 444 CGGGACACCGGAGCATCTTCCCGCATGAGAACCTCAACGCGGCGCTGGCCAAACGC 503
QY 438 CGGCTTTCAGAACATCAAGGTCTCCACATCAGTCTCTCTTCGGCGGTGCTGCGTACCTATA 497
DB 504 CGGCTGCGGCGGAGCATCAAGGTGTCACGCGGTGTCAGAGCGAGGTCAACGAGGCTT 563
QY 498 TCCCGCTCAGCTGCGCTCTCTCTTCGGATGCGATGCTCGACATTTGGGTCCAATACATA 557
DB 564 CCGCGCGTGCAGGGGACCTTCTCGCAGGGCTACATGCGG-----CCCATCGCGCA 614
QY 558 GTTCTAGCCAGCAATGCTCCCATTAATTTGCGCAACATCTACCCCTACTTTGAGCTATGC 617
DB 615 GTACTGAGAGCACCGGCGCGCTGCTGTGAACTGTACCCCTACTTCTCTCTACAT 674
QY 618 TGGCACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACTGTCATCTGGTACAGTCGT 677
DB 675 CGGCAACCGGCGGAGATCGACCTCAGCTACGCGCTCTTCACTCGCGGCGACCGTGT 734
QY 678 ACAGACCGGTCTTACGCTTACAAACCTCTTTCGATGCGCATGCTCGAGCGATTTGACTC 737
DB 735 GCAGGACGGCAGCAACGCTTACAGAACCTCTTCGACGCGCTCGTTCGACACCTTCTGCTC 794
QY 738 GGCCTGAGAGCGCGGAGGCGCAATGTCCTGTTGCTGTCGGAGAGTGGCTGGCC 797
DB 795 CGCGCTCAGAACCGCGCGCGCGGCAACGTCCTGCTGTCGTCGAGAGCGGCTGGCC 854
QY 798 GTCAAGCGCGGAGCAGCGCGCGCTGTCTAATGCGCAGACTTACAAATTTCAATTTGAT 857
DB 855 GTCCGCGGGGCGACGCGCGCGCACCGGCGCAACGCGCAGACCTACAAACCAAGACCTCAT 914
QY 858 CAACATGTTGGGTGAGGGGAGCGCGAGAGCGCGGCGGCGATTTGAGACCTACATTTTGC 917
DB 915 CAACCATGTCGCGGCGGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 974
QY 918 CATGTTCAACGAGATCAGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 977
DB 975 CATGTTCAACGAGACCGAGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1034
QY 978 CCCTAACGAAACAGCGCTGTCTATTGATCAGCTTCACTTGA 1017
DB 1035 CCGGACAAATCGCGGCGGTACCCCATCAATTTCTCTCTAA 1074

RESULT 13
AAQ24290
ID AAQ24290 standard; DNA; 4643 BP.
XX
AC AAQ24290;
XX
DT 02-NOV-1992 (first entry)
XX
DE (1-3,1-4)-beta-glucanase isoenzyme EI.
XX
KW Distal promoter; proximal promoter; introns; signal peptides; EI;
KW beta-glucan; endospore; beer production; ss.
XX
OS Hordeum vulgare.
XX
FH Key Location/Qualifiers
FT TATA_signal 420..430
FT /*tag= b
FT /*note= "Distal promoter, see comments"
FT misc_signal 474
FT /*tag= c
FT /*label= Transcription_start_point

CDS /note= "Distal promoter"
546..4064
/*tag= a
/label= E1
546..3143
/*tag= e
/note= "Distal promoter, see comments"
619..3132
/*tag= d
/note= "Distal promoter, see comments"
836
/*tag= g
/label= Transcription_start_point
/note= "Proximal promoter"
297..2807
/*tag= f
/note= "Proximal promoter, see comments"
3020..3143
/*tag= i
/note= "Proximal promoter, see comments"
3078..3132
/*tag= h
/note= "Proximal promoter, see comments"
3144..4061
/*tag= j
/label= E1
4399..4404
/*tag= k
/note= "Both promoters"

Query Match 33.8%; Score 380.8; DB 2; Length 4643;
Best Local Similarity 64.2%; Pred. No. 7e-87;
Matches 606; Conservative 0; Mismatches 332; Indels 6; Gaps 2;
QY 75 AGCGCTGGGAATCATTTGGGGTCTGCAATGGAATGGAAGGAGCAAACTCCCCAGGCCGC 134
Db 3131 AGCGCTGGAGTTCATCGGGGTGTGCTACGGCATAGCGCAACAATCTGCGCGCGAG 3190
QY 135 CGACGTCTCAACCTCTACAAGTCCAAACAACATAGCTGGCATCGCATCTTACAGCCCCGA 194
Db 3191 CACCGTGGTCAACATGTTCAAGTCCAAACGGGATCAACTCCATGCGGTGTACGCTCCGA 3250
QY 195 CCAAGCCTCTCCAGGCCCTCCAGGGCTCTTAACATCTACCTCATCTCGAGCTGCCCAA 254
Db 3251 CCAGCGCGCTGCGAGCGGTGCGGCGCACGGCGGTGAACGTTGTTGGCGCGGCCAA 3310
QY 255 CTCGACCTCCAAACATTTGCTCCGACCAATCCGCGGCCCAACAACTGGGTCCAAACCA 314
Db 3311 CGACGTGCTCTCAACCTCGCGGCAGTCCCGAGCGGTGCATCGTGGGTGAGGAGCAA 3370
QY 315 CGTCCAAGCTTACCCAAACGTTGCTTCGATATACATCGCGCTCGGAACGAAAGTCAATCC 374
Db 3371 CATCCAGGGTACCCCAAGGTCTCTTCGGGTATGCTTCGGTGGGCAACAGG---TCGC 3427
QY 375 CGCGCGCCAAGCTCAGTACGTCTCTCCAGCCATGAACAACAATACAGTCCGCCCTCTCCTC 434
Db 3428 CGCGCGGCCACCCAGAACCTTTGTCCTCCGCGCATGAAGAGGTGAGGGCGCGTGGCCTC 3487
QY 435 TCGCGGCTTCAGAAATCAAGGTCTCACAATAGTCTCTCTCGGGTGTGGGTACCTC 494
Db 3488 CGCGCGGTGGGCCACATCAAGGTGACCAAGTCTCGGTGTGCGAGGCCATCTCGGGGTGA 3547
QY 495 ATATCCCCCTCAGCTGGCTCTCTCTTCGATGATCGCTCGACATCGGTCCCAATCAT 554
Db 3548 CAGCCCGCGCTCCGCGGTCTCTTACCGAGAGGCGGAGCGGCTTCATGGGCCCGCTG 3607
QY 555 ACAGTTTCTAGCCAGCAATGGCTCCCAATTAATTGCCAACATCTACCCCTACTTTGAGCTA 614
Db 3608 GCAGTTCTTGGCGCGCACCGCGCTCATGCGCAACATCTACCCGTACTTGGCCTG 3667
QY 615 TGCTGGCAACTCCGGATCATCGACTCTCTCATACGCCCTCTTTTACTGATCTGGTACAGT 674
Db 3668 GGCCTACAAACCGAGCGCATGGAATGAGCTACGCGTCTTTCACGCGCTCCGGCACCGT 3727
QY 675 CGTACAGACGGTCTTACGCTTACAAACCTCTTCGATGCCATGGTTCGAGCATGTA 734
Db 3728 GGTCCAGACGGCTCTTACGGGTACGAACCTGTTCCGACACCCGCTGAGCGCTCTTA 3787
QY 735 CTCGGCCCTGAGAGCGCGGAGGCGCAATGTCCTGTGTGCTGTCGAGAGTGGCTG 794
Db 3788 CACGGCCATGGCCAGCAGCGGGGCTCCAACTGAGCTGGTGTGTCGAGAGCGGGTG 3847
QY 795 GCGGTACGCGGGCGGAGCAGCGGCGACGGTGTCTTAATGCGCAGACTTACAAATTCCAATTT 854
Db 3848 GCGGTACGCGGGCGGACGCGGCGGACGCCGCGCAACCGCGCAACGAGGATCTACAAACGAGTACCT 3907
QY 855 GATCAACCATGTGGTTCAGGGGAGCGCCGAGAGGCGGAGGCGGATGAGACCTACATATT 914
Db 3908 CATCAACCATGTGCGGGCGCGGCGCCCGCGCACCGCGGCGCATCGAGACCTAGCTCTT 3967
QY 915 TGCCATGTTCAACGAGGATCAGAACGCGCGCAAGGGATTGAGATAACTTTGGGCTGTT 974
Db 3968 CTCATGTTCAACGAGAACCGAAGGA---CAACGCGGTGGAGCAGAACTGGGGGCTCTT 4024
QY 975 TTACCTTAACGAGCGCTGTCTATTTCGATCAGCTTTCATTGAG 1018
Db 4025 CTACCCCAACATGAGCAGCTCTACCCCATCAGCTTCTGATGAG 4068

RESULT 14
ADL18243
ID ADL18243 standard; DNA; 4849 BP.
XX

This sequence encodes (1-3,1-4)-beta-glucanase isoenzyme E1 gene, showing the two promoter regions, the distal and proximal promoters. The two transcripts produce the same mature protein but have different signal peptides. The transcript from the distal promoter is 4169bp long and contains an intron of 2513bp. This intron is unusually long for a plant intron which have an average length being 249bp. The signal peptide produced from this transcript is 28 amino acids long. The transcript from the distal promoter is 3807bp and contains an intron of 54bp. The signal peptide produced from this transcript is 23 amino acids long. There is some evidence that suggests that these differing introns may have some role in exon "shuffling". E1 is synthesized in germinating barley grain where it acts to depolymerise the beta-glucans in the cell walls of the starchy endosperm. Low levels of the enzyme leads to high levels of the glucans and this can cause a reduced malt quality, serious filtration difficulties in the brewing process and can contribute to haze formation in the final product. The isolated E1 gene can be transferred to plants to generate varieties which have improved malting and brewing properties. Alternatively the gene can be introduced into yeast to remove residual beta-glucan in beer prodn. This protein can be mutated to generate a more thermostable enzyme

Sequence 4643 BP; 1166 A; 1190 C; 1110 G; 1177 T; 0 U; 0 Other;

AC ADL18243;
XX 06-MAY-2004 (first entry)
XX Barley gene sequence.
XX barley; wheat; chromosome 1H; fertility; gene; ds.
XX Hordeum vulgare.
XX JP2003111593-A.
XX 15-APR-2003.
XX 04-OCT-2001; 2001JP-00309184.
XX 04-OCT-2001; 2001JP-00309184.
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2003-601767/57.
XX Novel primer set for detecting nucleic acid markers derived from long arm
XX of 1H chromosome of barley on wheat genetic background.
XX Disclosure; Fig 1-3; 27pp; Japanese.
XX The invention relates to a novel primer set (I) for detecting barley
XX nucleic acid markers on wheat genetic background. The primer set is
XX useful for detecting nucleic acid markers derived from barley chromosome
XX on wheat genetic background. The primer set is useful for determining
XX whether the long arm of 1H chromosome of barley has been introduced into
XX wheat, and for determining fertility of wheat. The method enables
XX detection of nucleic acid markers derived from long arm of 1H chromosome
XX of barley on wheat genetic background. The present sequence represents a
XX barley gene used to design PCR primers ADL18230 and ADL18231 of the
XX invention.
XX Sequence 4849 BP; 1260 A; 1217 C; 1119 G; 1253 T; 0 U; 0 Other;
Query Match 33.8%; Score 380.8; DB 10; Length 4849;
Best Local Similarity 64.2%; Pred. No. 7,1e-87;
Matches 606; Conservative 0; Mismatches 332; Indels 6; Gaps 2;
QY 75 AGGCGTGAATTCATTTGGGGTCTGCAATGGAATGACGGTGACAACTCCCGGAGCCCGC 134
Db 3531 AGGCGTGAATTCATTTGGGGTCTGCAATGGAATGACGGTGACAACTCCCGGAGCCCGC 3590
QY 135 CGACGTGCTCAACCTCTACAGTCCAAACAAACATAGCTGGCATCTACAGCCCGCA 194
Db 3591 CACCGTGTCAACATGTTCAAGTCCACCGGATCAACTCCATGCGGCTGTAGCTCCCGA 3650
QY 195 CCAAGCCACTCTCCAGGCGCTCCAGGCTCTAAACATCTACCTCATCTCGACGTCGCCAA 254
Db 3651 CCAGCGGGCTGACAGCGGTGGCGGCAACGGCGTGAACGTTGTTGGGGCGGCCAA 3710
QY 255 CTCGACCTTCCAAAACATTTGCTTCGACCAATTCGCGCGCCACCAACTGGGTCCAAACAA 314
Db 3711 CGACGTGCTCTCAACCTCCGCGCGGCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTG 3770
QY 315 CGTCAAGCCTTACCAAGCTTGGCTTCCGATACATCCGCTGCGAAGCAAGTCAATCC 374
Db 3771 CATCCAGCGGTACCCCAAGGCTCTCTCCGATGCTCTGCGTGGGCAACGAGG---TCGC 3827
QY 375 CGGCGGCGCAAGCTCAGTACGCTCTCCAGCCATGAACCAATACATAGTCCGCGCTCTCTC 434
Db 3828 CGGCGGCGCCACCAAGACCTTGTCTCCCGCATGAAGACGTTGACAGGGCGGCTGCGCTC 3887
QY 435 TGGCGGCTTCAAGACATCAAGGCTCTCAACATCACTCTCTCTGCGGCTGCTGCTGCTGCT 494
Db 3888 CGCGGGGCTGGGCGCAACAGGTTGACCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3947
QY 495 ATATCTCCCTCAGCTGGCTCTCTCTCTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 554

Db 3948 CAGCCCGCGTCCCGCGGCTCTTCAACGAGAGCGGACCGCTTCATGGGCCCCGCTGT 4007
QY 555 ACAGTTCTAGCCAGCAATGGCTCCCATATCTATTTGCAACATCTACCCCTACTTGAGTGA 614
Db 4008 GCAGTTCTTGGCGGACCGCGGCGGCTCATGGCAACATCTACCCGTAACCTGGCCTG 4067
QY 615 TGCTGGCACTCCGGATCCATCGACCTCTCATAGCCCTCTTTACTGCATCTGCTACAGT 674
Db 4068 GGCCTACAACCCGAGCGCCATGGACATGAGCTACGCGCTCTTACCCGCTCCGGACCGT 4127
QY 675 CGTACAGACCGGCTCTACGCTTACAACAACTCTTGGATGCCATGGTTCGACGCAATTTGA 734
Db 4128 GGTCCAGGACCGCTCTTACGCTTACGAGTACGAGTCTTTCGACACCAACGCTGGAGGCTTCTA 4187
QY 735 CTGCGGCTTGAGAGCGCGGAGCGGCGGCAATGTCCTGTTGCTGCTGCTGCTGCTGCTGCTG 794
Db 4188 CACGCGCATGGCCAAAGCAGCGCGGCTCCACGCTGAAGCTGCTGCTGCTGCTGCTGCTGCTG 4247
QY 795 GCGCTCAGCGGCGGAGCAGCGGCGGCTGCTTAATGCGGCGAGCTTACAATTTCAATTT 854
Db 4248 GCGCTCAGCGGCGGAGCAGCGGCGGCTGCTTAATGCGGCGAGCTTACAATTTCAATTT 4307
QY 855 GATCAACCATGCTGGGTCAAGGAGCGGCGGAGCGGCGGCTGCTTAATGCGGCGAGCTTACAATTT 914
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QY 915 TGCCATGTTCAACGAGGATCAAGAGCGGCGGAGCGGCGGCTGCTTAATGCGGCGAGCTTACAATTT 974
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QY 975 TTACCTTAACGAGGATCAAGAGCGGCGGAGCGGCGGCTGCTTAATGCGGCGAGCTTACAATTT 1018
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RESULT 15
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ID ADJ11803 standard; DNA; 1110 BP.
XX AC ADJ11803;
XX AC ADJ11803 (first entry)
XX 20-MAY-2004 (first entry)
XX Rice cDNA modulated by post-transcriptional gene silencing SeqID 439.
XX rice; gene; ss; post-transcriptional gene silencing; PTGS; plant;
XX trans-activation; cereal; plant-viral interaction.
XX Oryza sp.
XX US2003135888-A1.
XX 17-JUL-2003.
XX 26-SEP-2002; 2002US-00259165.
XX 26-SEP-2001; 2001US-0325277P.
XX 27-MAR-2002; 2002US-0368327P.
XX 04-APR-2002; 2002US-0370620P.
XX (ZHUT/) ZHU T.
XX (WANG/) WANG X.
XX (CHAN/) CHANG H.
XX (BRIG/) BRIGGS S P.
XX (COOP/) COOPER B.
XX (GLAZ/) GLAZEBROOK J.
XX (GOFF/) GOFF S A.
XX (KATA/) KATAGIRI F.
XX (MOUG/) MOUGHAMER T.
XX (PROV/) PROVANT N.
XX (RICK/) RIQUE D.

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 20:27:54 ; Search time 5216 Seconds
(without alignments)
10091.156 Million cell updates/sec

Title: US-10-647-649-2

Perfect score: 1125

Sequence: 1 ttcatggcagctcagcacat.....ctaattaaactataaata 1125

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: fgb_est3:*

4: gb_hc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435.2	38.7	1014	10	CL960506
2	410	36.4	1109	8	DR741429
3	392.8	34.9	1307	5	BUI03698
4	353.6	31.4	1005	10	CL971054
5	343	30.5	1107	7	CK210431
6	342.8	30.5	1025	7	CK162463
7	342.2	30.4	1014	10	CL960494
8	338.8	30.1	1134	7	CK161205
9	337.4	30.0	950	10	CG352135
10	335.6	29.8	1092	10	CL960507
11	335.4	29.8	1020	10	CL982353
12	328.2	29.2	1005	10	CL960504
13	327.6	29.1	927	10	CG450991
14	320.4	28.5	1005	10	CL960493
15	313.2	27.8	1017	10	CL959613
16	312	27.7	919	10	CG203193
17	307.4	27.3	764	5	BQ801977
18	304.8	27.1	1587	10	CL947558
19	303.2	27.0	4248	10	CL960511
20	302.6	26.9	823	7	CK201565
21	302.4	26.9	891	10	CM027959
22	301.6	26.8	840	6	CB673940

23	301.4	26.8	729	1	AJ613783
24	300.2	26.7	966	10	CL960877
25	299.6	26.6	858	8	CV766157
26	296.2	26.3	812	7	CK201895
27	296.2	26.3	1015	8	DR738420
28	295.4	26.3	781	9	CG646871
29	294.8	26.2	814	6	CB670194
30	292.8	26.0	751	2	BF265541
31	291.8	25.9	809	6	CB654106
32	291.8	25.9	861	6	CB644222
33	290.6	25.8	790	6	CF554537
34	290.6	25.8	1123	8	DR741036
35	290.4	25.8	817	6	CB670461
36	290.2	25.8	1033	7	CK214755
37	288.2	25.6	947	9	CG643933
38	288	25.6	790	6	CB653421
39	285.4	25.4	780	6	CB656551
40	285.4	25.4	805	6	CB657342
41	284.6	25.3	1096	8	DR739897
42	283	25.2	791	6	CB651782
43	283	25.2	828	6	CB670919
44	282.8	25.1	731	10	CL158546
45	282.4	25.1	790	6	CB652908

ALIGNMENTS

RESULT 1
LOCUS CL960506
DEFINITION CL960506 Oryza sativa (indica cultivar-group)
ACCESSION CL960506.1 GI:52375716
VERSION GSS.
KEYWORDS Oryza sativa (indica cultivar-group)
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
REFERENCE 1 (bases 1 to 1014)
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
1..1014
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

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Best Local Similarity 65.8%; Pred. No. 4.4e-107;
Matches 667; Conservative 0; Mismatches 338; Indels 9; Gaps 2;
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DB 1 ATGGCAAGCATGGTGTGCTTTTCATTTAACTGGCATGCTCTTGGAGTACTTCG 60


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Db 61 GTCACTCCTAAAGTGTGCAATCCATTGGCGTGTGTCTACGGCGTGAACCAACACCTG 120
QY 124 CCCAGCGCGCGAGCGTCAACTCTACAACTTCAAGTCCCAACATAGCTGGCATGGACTC 183
Db 121 CGTGCAGAGGAGCGTGTGAGCTCTACAGTCTGAAGGGATGCAATCCATGGGCATC 180
QY 184 TACAGCCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTTAACATCTACTCTCATCTC 243
Db 181 TACTTCCGAGGAGCGACATCTCCAGCGACTTAACCGGCTCAACATCGCCCTCACCATG 240
QY 244 GAGTCCCACTCGACCTCCAAACATTGCTCTCGACCAATCCGCGCCGACCAACTGG 303
Db 241 GGCGTGCACACGAGAACCTCTCCGCGTTCGCTCCGACCCCTCCGCGTGGCCAAATGG 300
QY 304 GTCCAAACCAAGCTCCAGCGCTTACCACAAAGTTGCTTCCGATACATCGCGTGGGAAC 363
Db 301 GTCAAGGAGACGTTCCAGGTCTACCCGGCGTCAACTTCCGCTACATCGCGCTCGGCAC 360
QY 364 GAAGTCACTCCCGGGCGCAAGCTCAGTACGTCTCTCCAGCCATGAACCAATACAGTCC 423
Db 361 GAGG---TTGAGAGCGCAACAGCGCAGAACTCTCTCCGSCCATGCAAAATGAACAGC 417
QY 424 GCGCTCTCTCTCGCGCTTCAGAACATCAAGAGTCTCCATCATAGTCTCTCTCGGCGTC 483
Db 418 GCGCTCTCTCGCTCGCGCTTCAGAACATCAAGAGTCTCTCTCGGTTCTCCGAGAGGCG 477
QY 484 GTCGCTACTCATATCCCCCTCAGCTGGCTCTCTCTCTCGATGATCGTGCACATTG 543
Db 478 GTGCTCGCGGGTACCCGCGTTCATGGCATGTCTCTCCCGAGAGCACTCTGATCATG 537
QY 544 GGTCCAAATACATACAGTTTCTAGCCAGCAATGGCTCCCATTTACTTGGCAACATCTACCCC 603
Db 538 ACGCCCATCGGAGTACTGTGGAGCACCGGGCGCGCTGATGGCCAAAGTCTACCCC 597
QY 604 TACTTGAGCTATGTGGCAATCCCGGATCCAT-----CGACCTCTCATAGCGCTCTTT 657
Db 598 TACTTTCGCTACGTGGGCAACCTCGGGGCCAGATCGACGACATCAACTAGCGCGCTCTTC 657
QY 658 ACTGCATCTGGTACAGTCTGACAGAGCGGTCTTACGCTTACAACTTACAACTCTTCGATGCC 717
Db 658 ACGTCCCGGACAGTGTGTCGAGACGGCGAGAGGCTTACCGAACTGTTGAGCGCC 717
QY 718 ATGCTCGACGCAATGTACTCGGCCCTGAGAGCGCGGAGGCGCAATGTCTCTCTGTTGTC 777
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QY 778 GTGTCGAGAGTGGCTGGCGCTGAGCGGCGGAGACAGCGGCGACGCTGTCTAATGCGGAG 837
Db 778 GTGTGGGAGAGCGGGTGGCGCTCGCGCGCGGCGACGCGGCGGAGCGCGCAGCAACGCGCAG 837
QY 838 ACTTACAATTCCAATTTGATCAACCATGTGGTCTAGGGGAGCGCGAGAGCGCGAGGSGC 897
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QY 898 ATTGAGACCTACATATTTGCAATGTTTCAACAGGAGTCAAGAGCAGCGCCCAAGGAGTTGAG 957
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QY 958 AATACTTTGGCGTGTGTTTACCTTAACGAAACAGCGCTGTCTTATTCGATCAGGTTTC 1011
Db 958 AGGCACCTTCGCGCTCTTCAACCGCTGATCAGTTCGCGCGGCTCACCATTAATTTTC 1011
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RESULT 2
DR741429 1109 bp mRNA linear EST 18-JUL-2005
LOCUS FGAS030484 Triticum aestivum FGAS: Library 2 Gate 3 Triticum
DEFINITION aestivum cDNA, mRNA sequence.
ACCESSION DR741429
VERSION DR741429.1 GI:70971098
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EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 1109)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)
Contact: Patrick Gulick
Plant Molecular Biology
Concordia University, Department of Biology
7141 Sherbrooke St. West, Montreal, Quebec H4B 1R6, Canada
Tel: 514 848 2424 Ext 3407
Fax: 514 848 2881
Email: pgulick@alcor.concordia.ca
This sequence is the direct result of the Base calling software
phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [37,809].
Plate: STG1 row: F column: 10.
Location/Qualifiers
1..1109
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 2 Gate 3"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial
parts (crown and leaf) of wheat cultivar Norstar from
control and long exposure times to low temperature. 4 mRNA
populations were combined before constructing the library;
7 days non-acclimated plants and 1, 23, and 53 days
cold-acclimated at 4C. Non-acclimated and cold-acclimated
plants were grown in vermiculite This is the only library
that was done according to the Invitrogen manual, and
therefore, a percentage of clones will not have the 3
prime end because of NotI digestion within the cDNA."

ORIGIN

Query Match 36.4%; Score 410; DB 8; Length 1109;
Best Local Similarity 66.8%; Pred. No. 3.3e-100;
Matches 635; Conservative 0; Mismatches 301; Indels 15; Gaps 3;
QY 21 CATCTCATGGCTGCCATGGCATCCCTCTTGTAGTACTCTCGGCAATCCGAGGGCGT 80
Db 66 CATGTTTTCGGTGGCGTGTGGCCCTTCTTGGAGTGTCTCTGGCATCCATTCTACAACGGT 125
QY 81 GGAATCCATTGGGGTCTGCAATGGAATGGAACGGGTGAACACCTCCCGAGCGCGCGACGT 140
Db 126 GCAGTTCATCGCGTGTGTCTACGAGTGAACGGCGACGGCTTGCCCTCGGCCAGCGAGT 185
QY 141 CGTCAACCTTCAAGTCCAAACAATAGTGGCATGCACTCTACAGCCCGGACCAAGC 200
Db 186 GGTGAGCTCTTACAGTCCAAACGGCATCACGGCGATGCGCATCTACTTCCGGACGCCAA 245
QY 201 CACTCTCAGGCCCTCCAGGGCTTAAACATCTACTCTCTCGACGTCCCGAATCCGA 260
Db 246 CGCCCTCGAGGCCCTCGAGCGCAGCAACATCGGCTCATCTGTCAGCGTGGCCAAACGAGA 305
QY 261 CCTCAAAAACATTGCTCCGACCAATCGCGCGCACCAACTGGGTCCAAAACCAAGTCCA 320
Db 306 CCTCGCTCCCTCGCTCCGACCGCTCGCGCGCACCGCTTGGGTCCAGACCAAGTCA 365
QY 321 AGCTTACCCAAACGTTGCTTTCCGATACATCGCGTCCGAAACGAAGT---CATCCCCGG 377
Db 366 GGCCTACGAGGGCTCAACATCAAGTACATCGCGCGCGGTAAACGAGTGGGCGACAGGG 425
QY 378 CGGCCAAGCTCAGTACGTCTCTCCAGCCATGAACACATCAGTCCGCGCTCTCTCTGC 437

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Db      426  CGCGGACACGGGAAACATCTCCCGGCATGCGAAGACCTCGAGCGCGCACTCTCCGCGGC 485
Qy      438  CGGCTTTCAGAACATCAAGGTCTCCACATCAGTCTCTTTCGGGTGCTGGTACCTCATTA 497
Db      486  CGGCTCGCGGGGATCAAGGTCTCCACGTCGGGTCTCGAGGGGTGACC---ACGGGTA 542
Qy      498  TCCCCCTCAGCTGGCTCTCTTCTTCGATGCGATCGTGCAGATGGGTCCCAATCATACA 557
Db      543  CCGTCCTCCCAAGGCACCTTCTCGCGC-----GATACATGGGTCCCATAGCGCA 593
Qy      558  GTTCTAGCAGCAATGGCTCCCATATTCTTGGCAACATCTAGCCCTACTTGAAGTATGC 617
Db      594  GTACGTGGCCAGCACCGCGGCCCGCTGCTCGCCCAACGTGTACCCCTACTTCTCGTACGT 653
Qy      618  TGGCAACTCCGGATCATCGACTCTCATACGCGCTCTTTACTTGCATCTGTGTACAGTGT 677
Db      654  GACAAACAGGCGCAGATCGACATCACTACGCGCTCTTCAGTCCGCGGACCGTGT 713
Qy      678  ACAGGACGGGTCTTACGCTTACAAACACCTCTTCGATGCCATGGTTCGACGCAATGTACTC 737
Db      714  GCAGGACGGCGCAACGGGTACCAGAACCTGTTCGACGCCCTCTGACACGCTTCTACTC 773
Qy      738  GGCCTTGGAGAGCGCGGAGGGCGGAATGTCCTGTGTGTGTCGTGCGAGAGTGGCTGGCC 797
Db      774  CGCGCTGGAGAGCGCGCGCGCGAGCGTCAACGTGTGTGTGTCGAAAGCGGGTGGGC 833
Qy      798  GTACGCGGCGGACAGCGCGCGAGCGGTGCTAATGCGAGACTTCAATTCGAATTTGAT 857
Db      834  GTCCGCGCGCGGACAGCGCGCGACACACGACCAACGCGCAGAGCTCAACACCAAGCTGAT 893
Qy      858  CAACATGTGGGTTCAGGGGACCGCGAAGAGCGCAGGGCGATTGAGACCTTACATATTTGC 917
Db      894  CNAACATGTGACAGAGGACCGCCAGAGGCGCAGTGTGTCGAGGCTTACGTGTTCG 953
Qy      918  CATGTTCACAGAGATCAGAACGCGCGCAAGGGATTGAGAAATACTTTGG 968
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RESULT 3
BU103698/c
LOCUS      BU103698      1307 bp      mRNA      linear      EST 12-AUG-2003
DEFINITION SCURT1023806.g Saccharum officinarum mRNA (Nogueira,F.T.S)
SOURCE      Saccharum officinarum cDNA, mRNA sequence.
ACCESSION  BU103698
VERSION     BU103698.1 GI:32815029
KEYWORDS    EST.
SOURCE      Saccharum officinarum
ORGANISM    Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
            clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
            complex.
REFERENCE   1 (bases 1 to 1307)
AUTHORS    Nogueira,F.T.S., de Rosa,V.E. Jr., Menossi,M., Ulian,E.C. and
            Arruda,P.
            low temperature
            RNA expression profiles and data mining of sugarcane response to
            Plant Physiol. 132 (4), 1811-1824 (2003)
PUBMED     12913139
COMMENT     Contact: Nogueira FTS
            Bioinformatics Lab
            Organization for Nucleotide Sequencing and Analysis
            C.P. 6176, Campinas, SP 13083-970, Brazil
            Tel: 55 19 37881101
            Fax: 55 19 37881089
            Email: tebaldi@unicamp.br.
            Location/Qualifiers
            1..1307
            /organism="Saccharum officinarum"
            /mol_type="mRNA"
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Matches 645; Conservative 0; Mismatches 362; Indels 15; Gaps 2;

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Qy      64   GCAATCCGAGAGGCGTGGAAATCCATGGGGTCTCAATGGGAATGGACGGTGCACACCTC 123
Db      1162  GCCATTCTCAGAGAGTCAGTCCATCGCGGTGTCTACGGCGTGAACGGCGACAATCTG 1103
Qy      124   CCCAGCGCGCGAGCGTGTCAACCTCTCAAGTCCAAACACATAGTGGCATGCGACTC 183
Db      1102  CCGTCGGGAGCGAGCTGTGTGAGCTCTACCACTCCACGGCATCAACCTGTATGGCATC 1043
Qy      184   TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACCTCATCTTC 243
Db      1042  TACTTCCCGGACCAACACGGCTCAACGGCTCAGCGGAGGAGCAACATCGGGTGTATG 983
Qy      244   GACGTCCCAACTCCGACTTCCAAACATTTGCTCCGACCAATCCCGCCCAACCAACTGG 303
Db      982   GACGTGCCAACTCGGCCCTCTCTCGCTGGCTTCCGACCCGCGGCGCGGCCACGCTGG 923
Qy      304   GTCCAAACCAAGCTCAAGCTTACCAAAAGTGTGCTTCCGATACATCGCCGTCGGAAC 363
Db      922   GTGCAGAGCAACGTGAGCGTTCCCGGGGTCAACTTTCAAGTACATCGCCGTGGGCAAC 863
Qy      364   GAAGTATCCCGCGCGGCAAGCTCAGTACGTCTCCCGAGCCATCAACCAACATACAGTCC 423
Db      862   GAGG---TCTCGGGGGGATACCAACAGCATCTCTCCCGCCCATGACACACGTCAACTCC 806
Qy      424   GCCTCTCTCTCGCGGCTTTCAGAAACATCAAGGTCTCCACATCAGTCTCTCTTCGCGCTC 483
Db      805   GCGCTGGCCCAACGCGGGCTGGGGAACATCAAGGTGTCCAGCGCGTGCAGAGTGGGCTC 746
Qy      484   GTGGTACTCTCATATCCCCCTCAGCTGGCTCTTCTCTTCGATGCAATGTCGCAATG 543
Db      745   ACCAGGGGTATCCCGCGCTCGCAGGGCAGCTTCTCGAGGGGTAC-----ATG 698
Qy      544   GGTCAACATACAGTCTTAGCCAGCAATGGCTCCCATTTACTTGCACAACTATACCC 603
Db      697   GGCCCATCGCGCAGTACTCTTCAGAGCAGGGGTGCCCCGCTCTGCAACAGCTATACCCC 638
Qy      604   TACTTGAGCTATGTGCGCAACTCCGGATCCATCGACCTCTCATACGCTCTTTTACTGCA 663
Db      637   TACTTCTCTACAGGGCAACGAGGCCAGATCGACCTCAGCTACGCGCTCTTCACTG 578
Qy      664   TCTGTACAGTGTACAGGACGGGTCTTACCGTTTACAAACACCTTTCGATGCCATGTC 723
Db      577   TCGGAAACCGTCTGTGAGGACGGGCAACCGTACCAAGAACCTCTTCGACGCGCTCGTC 518
Qy      724   GACGATTTACTCGGCCCTGAGAGGCGCGGAGGGCGGAATGTCCTTGTGTCTGTGTCG 783
Db      517   GACACTTCTGTCTCGCGCTCGAGAACCGCGCGCGGGAACGTCGGGCTGTCTGTGTC 458
Qy      784   GAGAGTGGCTGGCGCTCAGCGCGGGGACAGCGGCGAGCGGTGTCTAATGCGCAGACTTAC 843
Db      457   GAGAGCGGGTGGCGCTGGCGTGGCGGACCGCGCCACACCGGGGNAACGCGCAGACTTAC 398
Qy      844   AATTCCAATTTGATCAACCAATGTGGTTCAGGGGACGCGCAAGAGAGCCAGGGCGGATTGAG 903
Db      397   AACCAGAACCTCATCAACCAATGTGGGAGGGCAGCGCCCAAGCGCCCTGGAGCCATCGAG 338
Qy      904   ACCTACATATTTGCCATGTTCAACAGGATCAGAGGACCGCGCAAGGATTTGAGATTAAC 963
Db      337   ACCTACATCTTTGCGCATGTTCAACAGGACCGAGGACCGCGGAGCTGAGACGCGAGGAC 278
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/clone_lib="Saccharum officinarum mRNA (Nogueira,F.T.S)"

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Db 217 GG 216

RESULT 4
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LOCUS OsIFCC021002 Oryza sativa Express Library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL971054
VERSION CL971054.1 GI:52396716
KEYWORDS GSS
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 1005)
AUTHORS Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
source
1..1005
location/Qualifiers
/oranism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN
Query Match 31.4%; Score 353.6; DB 10; Length 1005;
Best Local Similarity 60.8%; Pred. No. 7.5e-85;
Matches 613; Conservative 0; Mismatches 389; Indels 6; Gaps 2;

Qy 4 ATGGCAGCTCAGCATCATCTCCATGGTCCATGGCATCCCTCTTGTAGTACTCTCG 63
Db 1 ATGGGTAGCAAGGTGTAGCTCCCATTTTCGCTCTCGCATTCCTCTCGGTGCTTGGC 60

Qy 64 GCAATCCCGAGAGGGGTGAATCCATTTGGGGTCTGCAATGGAATGGAGCGTGACAACCTC 123
Db 61 TCCATCTCTCAAGAGGAGGAGCGATCGGGGTGTCTACGGCATGAGCGGAGCAACCTG 120

Qy 124 CCCCAGCCCGCGAGCGTGTCAACCTCTCAAGTCCAAACATAGCTGGCATGCGACTC 183
Db 121 CGCGCGGCGAGCTCGGTGTGGGGATGTACCGCTCCAAACGGCATCACGTGCGATGGCGCTG 180

Qy 184 TACAGCCCGGACCAAGCCACTTCCAGGCCCTCCAGGGCTCTAAATCTACTCTCTCTC 243
Db 181 TACGCGCGGACGAGCGCGCTGAGTGGTGGGCGGACGGGATCAGCGTCTGCTGTC 240

Qy 244 GAGCTCCCCCAACTCCGACCTCCAAACATTTGGCTCCGACCAATCCCGCGCAACCACTGG 303
Db 241 GCGCGGCCCAAGAGTGTCTTCAACTCTGCGCGGAGCCCGCGCGGCGGCGGTCTGG 300

Qy 304 GTCCAAACCAAGCTCCAGCTTACCCAAAGCTTTCCTCCGATACATCGCGCTCGGAAC 363
Db 301 GTGCGGAACAACATCAGCGCTTACCGCTCGGTGTGTTCCGGTACGTGCGCGTGGGAAC 360
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Qy 364 GAAGTATCCCGCGCGCAAGCTCAGTACGTCTCTCCAGCATCAACAAACATACAGTCC 423
Db 361 GAGG---TCGCGGGCGGCGCAAGCTCCAGCTTGGTCCCGGCATGGAGAAAGTTCGCGGC 417

Qy 424 GCGCTCTCTCTGCGCGCTTCAGAAATCAAGGTCTCCATCATAGTCTCTTTCGGCGTC 483
Db 418 GCGCTGTGTCTGCGGGGGCTGGGCGACATCAAGGTGACGAGCTGCGGTGTCGAGCGCTC 477

Qy 484 GTGGGTACTCATATCCCGCTCAGCTGGCTCTCTCTCTTCGATGTCATCTCGACATTTG 543
Db 478 CTGCGCGGTATACAGCCCGCTGTCGCGCGAGTTTACCGCGGAGTCCGAGCGGTTCATG 537

Qy 544 GGTCCAATCATATACAGTTTCTAGCCAGCAATGGCTCCCATTTACTTTGCCAAATCTACCCC 603
Db 538 GCGCCGCTCTGAGCTTCTGCGCGCACCGCGGCGGCTGCTCGCCAAACATCTACCCC 597

Qy 604 TACTTGAGTATGTGGCAACTCCGGATCCATGCACTCTCATAGCCCTCTTTACTGCA 663
Db 598 TACTTCTCTACACCTACAGCCAGCGGAGCTGCGAGCTCTCTACGCGCTCTTTCACCGCC 657

Qy 664 TCTGGTACAGTCGTACAGGAGGGTCTTACGCTTACACAACTTTTCGATGCCATGTC 723
Db 658 CCGCGCACCGTCTGTCAGGAGCGGCTTACCGGTACCCAGAACCTGTTCGACACCACTGTC 717

Qy 724 GACGATTTGTTACTCGGCTCTGAGAGCGCGGAGCGGCGGCTTCCCTGTTGTCGTGTCG 783
Db 718 GACGGTTTCTAGCGCGCATGCGCAGCAGCGGCTCGGGGCTCTGCTGCTCTCTCC 777

Qy 784 GAGAGTGGCTGGCGCTCAGCGCGGAGCAGCGCGGAGCGGTGTCTTAATGCGCAGCTTAC 843
Db 778 GAGACAGGCTGGCGCTCGCGCGGCGGATGTCGCGCTCGCGCGCAACGCGCGGATCTAC 837

Qy 844 AATTCCAATTTGATCAACCATGTGGTCAGGGAGCGGAGAGAGCCAGGCGCGGATTCAG 903
Db 838 AACCCAGACCTCATCAACACGTCGCGCGGCGGAGCGCGCGCCACCCCGCGGCGCATCGAG 897

Qy 904 ACCTACATATTGTCATGTTCAACGAGGATCAGAGAGCAGCGCGCAAGGATTCAGAAATAC 963
Db 898 ACCTACGCTTCTTCATGTTCAACGAGAACCCAGAGGAGCGC---CGGGCTCGAGCAGAT 954

Qy 964 TTTGGGCTGTTTACCCTTAACGACAGCTCTCTATTTCGATCAGCTTC 1011
Db 955 TGGGGCTCTTCTACCCCAACATGCGACAGCTTACCCCATCAGCTTC 1002

RESULT 5
CK210431
LOCUS FGAS022241 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
DEFINITION aestivum cDNA, mRNA sequence.
ACCESSION CK210431
VERSION CK210431.1 GI:39572821
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 1107)
AUTHORS Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,
Penniket,C., Roach,J.L. and Sarhan,F.
Punical Genomics of Abiotic Stress In Wheat and Canola Crops
Unpublished (2003)
CONTACT: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_est@cs.usask.ca
```

This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [18,757].

Plate: L5B022 row: N column: 22.

Location/Qualifiers

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1. .1107
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"
/note="Vector: pCMV.SPORT6; Crown and developmental stages of spike formation in wheat cultivar Norstar. 4 mRNA populations were combined before constructing the library. The first mRNA population is from 1cm crown sections after 30 days of cold acclimation. The second is from 1cm crown sections after 11 days of deacclimation (before deacclimation plants were fully vernalized for 49 days). The third is from different developmental stages of spike formation (5 to 50mm) that still have not emerged from the leaf (dissection required). The last is from different developmental stages of spike and seed formation after having emerged from the leaf (visible). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."
```

ORIGIN

```
Query Match 30.5%; Score 343; DB 7; Length 1107;
Best Local Similarity 63.3%; Pred. No. 6e-82;
Matches 556; Conservative 0; Mismatches 319; Indels 4; Gaps 2;

QY 4 ATGGCAGCTCAGACATATCTCCATGCTGCTGCGATCGATCCCTCTCTGTAGTACTCTCG 63
DB |||||
QY 109 ATGGGAGGCAAGGTTGCTTCCATTTGCTCTGCGATTCCTCTCGGGCCTTCGCG 168
DB |||||
QY 64 GCAATCCCGAGAGGCGTGAATCCATTTGGGGTCTGCAATGGAATGGAGCGTGCAACCTC 123
DB |||||
QY 169 TCCATCCCAAAAGCGTGAGTCCATCGAGTGTGTCAGGCGATGAGCGCAACACCTG 228
DB |||||
QY 124 CCCCAGCCGCGAGTGTGTAACCTTCAAGTCAACATAGTGGGATGGAGTGC 183
DB |||||
QY 229 CCGGCGGCGAGCAGCGTCTGAGCATGTTCAAGTCCAAGCGCATCAACTCCATCGCGGTG 288
DB |||||
QY 184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGCTTAAATCTACTCTATCTCTC 243
DB |||||
QY 289 TACGCCCCGACGAGCGCGCTGCGAGCGCGTCCGCGGACCGCGGTCAACGTCTGCTGTC 348
DB |||||
QY 244 GACGTCCCCCACTCCGACCTCCAAACATTTGCTCTCGACCAATCCGCGGCCCAACACTGG 303
DB |||||
QY 349 GGGGCGCTTAAGAGTGTCTTCCAACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 408
DB |||||
QY 304 GTCCAAACCAAGCTCAAGCTTACCAAGCTTCCGATATCATCGCGTCCGGAAC 363
DB |||||
QY 409 GTCCAGAGCAACATCAGCGCTTACCCCAAGGTCTCTTCGCGTACGTCTGCGTCCGCAAC 468
DB |||||
QY 364 GAGGTATCCCGCGGCGCAAGCTCAGTACGTCTCTCCAGCCATCAACATACAGTCC 423
DB |||||
QY 469 GAGG---TCGCGCGCGCGCGCACCCAGAACCTCTGCTCCGCGGCATGAAGACGTGCGGGC 525
DB |||||
QY 424 GCGCTCTCTCTGCGCGGCTTCAGAACATCAAGGTCTCCACATCAGTCTCTCTGCGCGTC 483
DB |||||
QY 526 GGGCTCGCTCGCTGGGTGGGCGACATCAGGTCAACAGTGTGCGGTCGCGAGGCCATC 585
DB |||||
QY 484 GTCCGATCTCATATCCCGCTCAGTGGCTCTCTCTCTTCGATGTCATCGTCGACATG 543
DB |||||
QY 586 CTCGCGGTGTACAGCGCGCTTCCGCGGTCTCTTACCGGGAGGCGGCGGCTTCATG 645
DB |||||
QY 544 GGTCAATCATACATTTCTAGCCAGCAATGGCTCCCATTTACTTGGCCAAATACCCCC 603
DB |||||
QY 646 GGACCGTGTGGTCACTTCTTGGCGGCGCGCGCGCGCTCATGGCCCAACATCTACCGG 705
DB |||||
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QY 604 TACTTGAGCTATGCTGGCAATCCCGATCCATGACCTCTCATACGCCCTCTTTACTGCA 663
DB |||||
QY 706 TACTTGGCTGGGCTCTACAAACCGGAGCGCATGAGCATGAGCTACGGCTCTTTCANCGG 765
DB |||||
QY 664 TCTGCTACAGTCTGATCAGGAGCGGTCTTACGCTTACACCACTCTTTCATGCTGCTGTC 723
DB |||||
QY 766 TCCGGCACCGTGGGTGAGGACGGCTCTTACGGGTACCAAGNNAACTGTTCGACACCAACG 825
DB |||||
QY 724 GACGCAATTTACTTCGGCCCTGAGAGAGCGCGGAGCGCGGAAATGTCCTCTTGTGCTGTCG 783
DB |||||
QY 826 GAGCGCTTCTACACGGCCATGSCCAAGCACGCGGCTCCACAGTGAAGCTGTGTGTGTC 885
DB |||||
QY 784 GAGAGTGTGCTGCTCAGCGCGGAGCAGCGGAGCGGTGTCTTAATCGCAGACTTAC 843
DB |||||
QY 886 GANAGCGGTGCGCTGCGGGGCGGACGCGGCGGAGCCCGCGCAACGCCAGGATCTAC 945
DB |||||
QY 844 AATTCATTTGATCAACATGTGGTTCAGGGAGCGCG 892
DB |||||
QY 946 AA-CAGTACCTCATCAACACGAGTGGGCGCGGACCCCG 983
DB |||||
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RESULT 6

CKL62463

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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CKL62463 1025 bp mRNA linear EST 05-DEC-2003
FGAS015057 Triticum aestivum FGAS: Library 4 Gate 8 Triticum
aestivum cDNA, mRNA sequence.
CKL62463
CKL62463.1 GI:38991695
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1025)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, P., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Larocque, A.,
Lins, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, P.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas.est@cs.usask.ca
```

This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [27,866].

Plate: L4B005 row: A column: 08.

FEATURES

source

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1..1025
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6;
Conditions for growth: Seeds were germinated in a
water-saturated mix (50% black earth and 50% Promix) in a
growth chamber for 7 days under an irradiance of 200 mmol
m-2 sec-1. The temperature was maintained at 20 degrees C
with a 15-hr photoperiod under a relative humidity of 70%.
After this period watering of plants was stopped. Four
time points were sampled during a two week period; the
first after wilting was observed and the last, two weeks
later, consisted of live crown and leaf tissue (leaf
tissue that was yellow was not included in sampled
material). First strand synthesis in this library was done
```



```
Qy      844 A 844
Db      912 A 912

RESULT 9
CG352135
LOCUS   CG352135
DEFINITION  CG352135 950 bp DNA linear GSS 26-AUG-2003
            OGI:BTITV ZM_0.7_1.5_KB Zea mays genomic clone ZMBMa0726A22,
            genomic survey sequence.
ACCESSION  CG352135
VERSION    CG352135.1 GI:34269401
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
REFERENCE  1 (bases 1 to 950)
AUTHORS    Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Frazer,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
            Citeck R.W., Nurnberg A., Robbins D. and Lakey N.
            Consortium for Maize Genomics
            Unpublished (2002)
            Other GSSs: OGI:BT11TH
            Contact: Cathy Whitelaw
            TIGR
            712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TP
            Class: methylation filtered.
            Location/Qualifiers
            1..950
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
            /clone="ZMBMa0726A22"
            /clone_lib="ZM 0.7 1.5 KB"
            /note="Vector: pBOSK; Site 1: HincII; 0.7-1.5 kb
            methylation filtered genomic DNA library"

FEATURES
            source
            1..950

ORIGIN
Query Match 30.0%; Score 337.4; DB 10; Length 950;
Best Local Similarity 61.9%; Pred. NO. 1.9e-80;
Matches 571; Conservative 0; Mismatches 346; Indels 6; Gaps 2;

Qy      75 AGGCGTGGAATCCATTGGGGTCTGCAATGGATGGAACGGTGACACCTCCCGGAGCCCGC 134
Db      34 AGGTGCTAGAGCCATCGGGGTGTGCTACGGCATGAGCGCCCAACACCTGCGCGGGCGAG 93
Qy      135 CGAGCTGCTCAACCTCTCAAGTCCAAACATAGCTGCGATGCGACTCTACAGCCCGGA 194
Db      94 CACGGTGTGAGCATGTAAAGGCGAAGCGGCATCTCGCGGATGCGGCTGTACGGCGCGGA 153
Qy      195 CCAAGCCACTCTCCAGGCGCTTCCAGGGCTCTAAACATCTACCTCATCTCGACGTCGCCAA 254
Db      154 CCAGGGCGCTCGACGGCGGTGGCGGCGACGGGCATCAGCTGGCGGTGGCGGCCCGCAA 213
Qy      255 CTCGACCTCCAAACATGTGCTTCGGACCAATCGCGCCGACCAACTGGGTCCAAACAA 314
Db      214 CGACGTGTGTCACATCGGGCTAGCCCGCGCGCGCGCTGCTGGGTGCGCAACAA 273
Qy      315 CGTCAAGCTACCCAAACGTGTGCTTCGGATACATCGCGTCCGAAACGAAGTCATCCC 374
Db      274 CATCAGGGGTACCGCTCGTGTGCTTCGGTACGTGTGCGTGGGCAACGAGG---TGGC 330
Qy      375 CGGCGGCCAAGCTCAGTACGTCTCTCCAGCCATGAAACACATACAGTCCGCCCTCTCTC 434
Db      331 CGGCGCGCGGCGCAGGACCTTGGCGCGGCCATGAGAACGTGCACGGCGGCTGGCGGC 390

            435 TGCGGGCTTCAGAAACATCAAGGTCTCCACATCAGTCTCCTTCGGCGCTGCGGTACCTC 494
            391 GGGCGGGCTGGCCACATCAAGGTGACGACGTGGTGTGCGAGGCCATCTTGGGGGTGTA 450
            495 ATATCCCCCTCAGCTGGCTCTTCTTCCGATGCATCGTCGACATTTGGGTCCAATCAT 554
            451 CAGCGCGCGCTCGCGCGGGAGTTTCA CGGCGAGCGCGCGGTACATGGGCCCGGTCT 510
            555 ACAGTTTCTAGCAGCAATGGCTCCCATTTACTTGGCAACATCTACCCCTACTTTGAGTA 614
            511 GCAGTTCTGCGCGCACCGGGTCCGGCTCATGGCCAAACATCTACCGGTACCTGGCCTG 570
            615 TGCTGGCAATCGGATCTCATCGACCTCTCATAGCCCTCTTTACTGTCATCTGGTACAGT 674
            571 GGCATACACCCAGCGCATGAGCATGAGCTACGGCTCTTCACTCTCTCCGCCACCGT 630
            675 CGTACAGGACGGGTCTTACGCTTACAAACAACTCTTCCGATGCCATGTCGACGATTTGA 734
            631 CGTCAGGACGGGCTTACGGGTACCGGTACCGACCTCTTCCGACACCAACCGTTCGACGCTTCTA 690
            735 CTGCGGCTTGAGAGCGCGCGGAGGCGCAATGTCCTCTGTTGTCGTCGGAGAGTGGCTG 794
            691 CGTCGCATGGGCAAGAACCGCGGCTCCGGCTGCGCTCGTGGTGTGCGAGAGCGGGTG 750
            795 GCGCTCAGCGGGGAGACAGCGCGAGCTGCTCTAATGCGCAGACTTACAATTCCAATTT 854
            751 GCGCTCGCGGCGCGCTCGAGGCGACGCCGCCCAACCGGAGGTGTACACCGTACCT 810
            855 GATCAACCATGTGGTTCAGGGGACCGCGAAGAGAGCCAGGGCGGATTTGAGACCTACATATT 914
            811 CATCAACCATGTGGGCGCGGACCGCGCCACCGCGGCCATCGAGACCTACCTCTT 870
            915 TGCCATGTTCAACGAGGATCAGAGCAGCCCGCAAGGATTCAGAAATTAATTTGGGCTGTT 974
            871 CTCCATGTTCAACGAGAACCCAGAAAGA---GAGCGGGTGGAGCAGAACTGGGGGCTCTT 927
            975 TTACCCTAAGCAACAGCTGTCT 997
            928 CTACCCCAACATGAGCACGCTCT 950

RESULT 10
LOCUS   CL960507
DEFINITION  CL960507 1092 bp DNA linear GSS 21-SEP-2004
            OrlFCC04630 Oryza sativa Express Library Oryza sativa (indica
            cultivar-group) genomic, genomic survey sequence.
ACCESSION  CL960507
VERSION    CL960507.1 GI:52375718
KEYWORDS   GSS.
SOURCE     Oryza sativa (indica cultivar-group)
ORGANISM   Oryza sativa (indica cultivar-group)
REFERENCE  1 (bases 1 to 1092)
AUTHORS    Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.
            An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
            Unpublished (2004)
            Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.
            Location/Qualifiers
            1..1092
            /organism="Oryza sativa (indica cultivar-group)"

FEATURES
            source
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/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "

ORIGIN
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      Best Local Similarity 63.1%; Pred. No. 6.2e-80;
      Matches 594; Conservative 0; Mismatches 324; Indels 24; Gaps 4;

QY  71  CGAGAGGGGTGGAAATCCATTTGGGGTCTCGAATGGAATCGAGCGTGACAACTCTCCCCAGC 130
DB  164  CAAAGAGAGTGGCATTCATTCGGCGTGTGCAACGGCATATTTGGGGAACAACCTGCGGTGCG 223

QY  131  CGCCGCGAGCTCGTCAACCTCTCAAGTCCAAACAACATAGCTGGCATGCGACTCTACAGCC 190
DB  224  CGGCCGAGCTGTGTGAAGCTCTACCAAGTCCAAAGGCATCGCCGATCTACTCTCTCTCCC 283

QY  191  CGGACCAAGCCACTCTCAGGGCCCTCAGGGGCTTAAACATCTAATCTCATCTCTCGAGTCC 250
DB  284  CGACGCGCCCAACCTCGTGTGGCTTCGCGGCACCGACATCGCGCTCATCTGTCGACGAGC 343

QY  251  CCAACTCGGACCTCCAAACAATTGCTCCTCGGACCAATCGCCGCCACCAACTGGGTCCAAA 310
DB  344  CGGCCATCGACAAATTCCTCACT-----CTATCGCCGCATCAGACTGGGTTTCTGAG 394

QY  311  CCAAGCTCAAGCCCTAACCAAAAGTTGTCTTCGATACATCGCCGTGCGAAACGAAGTCA 370
DB  395  GCAACATCAAGCGGTACAGGGCGTCAACATCAGGTACATCGCGTGGGNAACGAGG--- 451

QY  371  TCCCGGGGGCGAAGCTCAGTAAAGTCTCTCCAGGCATGAACAACATACAGTCCGCCCTCT 430
DB  452  TGTCCGGCGAGCCACGCGGAGCATCTCTCCGGCCATGGAGAACTCACCAAGGCGCTGT 511

QY  431  CCTCTGCGGCTTCAGAAACATCAGGTCTCAATCAGTCTCTTTCGGGGTGTCTGGTAA 490
DB  512  CCGCGGCTGGCTTCGGCAAGATCAAGGTGTCCAGGGCGGTCAAGATGGACGTGTCTGGCA 571

QY  491  CCTCATATCCCCCTCAGCTGGCTCTTCTCTCCGATGCATCTGTCACATTTGGGTCCAA 550
DB  572  CCTGTCGCGCCCTCTCGGCGGCGAGTTCAGCGAG-----CGCCGCTCATGGCCCCCA 625

QY  551  TCATACAGTTTCTAGCAGCAATGGCTCCCCATTAATTGTGCAACATCTACCCCTACTTGA 610
DB  626  TCGGGAAGTTCTTGGCGAGCAACGGCTCGCGCTGCTGGCCAAAGTCTACCCCTACTTGG 685

QY  611  GCTATGTGGCAATCTCGGATCCATACGACTCTCATAGCCCTCTTTACTGTCAATCTGGTA 670
DB  686  CCTA-----CAAGGGCGGGGACGTGCACTCTCAACTTCGCCCTCTTCCAGCCGACCA 739

QY  671  CAGTCTGATACGGAAGGGTCTCTACGCTTACAAACCTCTTCGATGTCATGTCGAGCAT 730
DB  740  CGACGCTGGCCGACGACGCGACATACAGCAACATGTTGCCGCGATGGTGAACGCCA 799

QY  731  TGTACTCGGCCCTTGAAGGCGCGGAGGGCGGAATGTCCCTGTGTGCTGTCTCGGAGAGTG 790
DB  800  TGTACTCGGCGTTGAGAAAGGCGGGGAGCCGGGGTGGCGGTGCTGTCTGTCCGAGAGCG 859

QY  791  GCTGGCGCTCAGCGGGCGGACAGCGGCGACGCTGTCTAATGCGCAGACTTACATTTCCA 850
DB  860  GGTGGCGCTCGGCGCGGGCTTCGCGCGGACGCGGGAACAACGCGCGAGGTACAAACGAG 919

QY  851  ATTTGATCAACCATGTGGGTGAGGGGACGCGGAAGAGGCCAGGGGGGATTTGAGACTTACA 910
DB  920  GACTGATGACCATGTTGGCATGTTGGGACGCCCAAGAGGGCAGGCGCATGGAGCGGTACA 979

QY  911  TAATTGCCATGTTCAAACGAGGATCAGAAAGCAGCGCAAGGGGATTTGAATTAATCTTGGGC 970
DB  980  TAATTGCCATGTTCAAACGAGAAACGAGAAGGACGGGGACGAGACGGAGAGGCACTATGGGT 1039

QY  971  TGTTTTACCTTAACGAACAGCTGTCTATTTCGATCAGCTTCA 1012
DB  1040  TGTTCAACCCCGCAACAGTCGCGGCTGACCTATCAAGTTCA 1081

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Db 463 GTGAGTGGAGCTGATCACCGCCTCGTCCCTCGTCGCAGCGGTGTTTCGCCCGGAC 522
Qy 529 GCATCGTCGACATTTGGTGGTCAATATACAGTTTCTAGCCAGCAATGGCTCCCAATACTT 588
Db 523 CTGCAGCAGTTTCATGTTGCCATCGCAGTTCTCTCGCCAAACACCATGTCGCCGTGCTC 582
Qy 589 GCCACATCTACCCCTACTGCTGATGCTGCTGGCACTCCGATCCATGACCTCTCATAC 648
Db 593 GCCAACGTGTACCCCTACTTCCCTTACAGGAGCAACCCCGGAGCATCCCGCTCAACTAC 642
Qy 649 GCCCTCTTTACTGATCTGTGTACAGTC---GTACAGGACGGGTCTTACGCTTACAAAC 705
Db 643 GCCAGTTCCAGCGGGGACACACGGTGGAGGACACGACAGGGGCTCACCTACACCAAC 702
Qy 706 CTCCTTCGATGCGATGTCGACGCAATTTGATCTCGGCCCTGGAGAGCGCCGAGGCCGAAT 765
Db 703 CTCCTTCAGCGCATGTTGGACGCGGTGTACCGCGGCTGGAGAGGCGCGCGCGCGCG 762
Qy 766 GTCCCTGTGTGCTGTCGAGAGTGGCTGGCGGTACAGCGCGGGGACAGCGCGGACGGTG 825
Db 763 GTCCGCGTGTGTCGAGAGCGGGTGGCGGTGTCGCGGAGGGTTTCGCGCGGAACGTG 822
Qy 826 TCTAATGCGCAGACTTACAAATTTCCAAATTTGATCAACCATGTGGTTCAGGGGACGCCGAAG 885
Db 823 GAGAACGCGAGATCACACAGGGCGTGTATGCAACAGCTCAGAACGGGACGCCGAG 882
Qy 886 AGGCAGCGGGCGATTGAGACCTTACATATTTGCCATTTTCAACGAGGATCAGAGCAGCGC 945
Db 883 CGGCCCGGGCAGCTGGAGACGTACGTGTTCGCCATGTTCAACGAGAACCAAGAGCCCGG 942
Qy 946 CAAGGGATTGAGATTAATTTGGGCTGTTTACCTTACGACAGACCTGCTTATTCGATC 1005
Db 943 GATGAGACCGAGAGGCATTTTGGGCTCTTACCCCTGACAGACCGCGGTCTACCCGATT 1002
Qy 1006 AGCTTCACT 1014
Db 1003 AGTTTCT 1011

RESULT 12
LOCUS CL960504
DEFINITION OBFCC004627 Oryza sativa Expressed Sequence Library Oryza sativa (indica
VERSION CL960504
KEYWORDS cultivar-group) genomic, genomic survey sequence.
SOURCE CL960504.1 GI:52375712
ORGANISM Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1005)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
1..1005
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/mo_l_type="genomic DNA"
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Query Match 29.2%; Score 328.2; DB 10; Length 1005;
Best Local Similarity 61.9%; Pred. No. 6.3e-78;
Matches 630; Conservative 0; Mismatches 363; Indels 24; Gaps 6;
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Qy 124 CCCAGAGCCCGCGCAGCTCGTCAACTCTACAAGTCCAAACATAGCTGGCATGCGACTC 183
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Qy 184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACCTCATCTC 243
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VERSION
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KEYWORDS
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SOURCE
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  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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  1 (bases 1 to 927)
  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
  Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
  Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  Consortium for Maize Genomics
  Unpublished (2002)
  Contact: Cathy Whitelaw
TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
  Location/Qualifiers
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      /mol_type="genomic DNA"
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FEATURES
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    ORIGIN
      Query Match 29.1%; Score 327.6; DB 10; Length 927;
      Best Local Similarity 62.1%; Pred. No. 9e-78;
      Matches 570; Conservative 0; Mismatches 339; Indels 9; Gaps 3;

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LOCUS
DEFINITION
  OSIFCC004606 Oryza sativa Exress Library Oryza sativa (indica
  cultivar-group) genomic, genomic survey sequence.
ACCESSION
  CL960493
VERSION
  CL960493.1 GI:52375690
KEYWORDS
  GSS.
ORGANISM
  Oryza sativa (indica cultivar-group)
  Oryza sativa (indica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehnartoideae; Oryzeae; Oryza.
  1 (bases 1 to 1005)
  Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
  Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
  Wong,G.K.S., Deng,X.W. and Wang,J.
  An analysis of transcriptional regulation of the rice genome and
  its comparison to Arabidopsis
  Unpublished (2004)
  Contact: Chen Chen
  Department of Bioinformatic
  Beijing Institute of Genomics
  Chinese Academy of Sciences, Beijing 101300, China
  Tel: 86-10-80481559
  Fax: 86-10-80488676
  Email: chenchen@genomics.org.cn
  Rice genomic sequence.
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Search completed: April 7, 2006, 22:17:25
Job time : 5227 secs

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Best Local Similarity 66.2%; Pred. No. 1.4e-112; Indels 15; Gaps 3;
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; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; TITLE OF INVENTION: and Genes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1834 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-105-390-4
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Best Local Similarity 67.0%; Pred. No. 4.6e-110;
Matches 629; Conservative 0; Mismatches 298; Indels 12; Gaps 2;

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RESULT 3

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US-09-105-390-39
; Sequence 39, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Pettithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455,30
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; NAME/KEY: Coding Sequence
; LOCATION: 1...912
; OTHER INFORMATION:
; US-09-105-390-39
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Best Local Similarity 67.0%; Pred. No. 3.3e-108;
Matches 619; Conservative 0; Mismatches 293; Indels 12; Gaps 2;

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QY 268 AACATTGCTTCGACCAATCCGCGCCCAACCACTGGGTCCCAACCAAGTTCGACGCTTAC 327
Db 181 TCCCTCGCTTCGACCCCTTCGCGCCCGCGCTTCGTCGAGAACAAATTCAGGCGTTC 240
QY 328 CCAAAAGTTGCTTCGATATACATCGCCGTTCGAAACGAAAGTCAATCCCGCGCGCCAAAGCT 387
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QY 628 GGATCCATCGACCTCTCATAGCCCTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 687
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RESULT 4
US-08-457-797A-11
; Sequence 11, Application US/08457797A
; Patent No. 5689045
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; FILING DATE: June 1, 1995
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 18,839
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Hordeum vulgare
; STRAIN: L.
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..48
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1050
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /codon start= 49
; OTHER INFORMATION: /function= "glucanase"
; OTHER INFORMATION: /product= "preprotein of the glucanase GluG"
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1051..1235
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /note= "14 nucleotides at the 3' end not shown."
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1083..1088
; OTHER INFORMATION: /note= "potential polyadenylation signal"

; NAME/KEY: polyA_signal
; LOCATION: 1210..1215
; OTHER INFORMATION: /note= "potential polyadenylation signal"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 133..1050
US-08-457-797A-11
Query Match 30.8%; Score 346.2; DB 2; Length 1235;
Best Local Similarity 60.4%; Pred. No. 2.le-89;
Matches 611; Conservative 0; Mismatches 388; Indels 12; Gaps 2;
QY 4 ATGGCAGCTCAGCACATCATCTCCATGCTGCCATGGCATCCCTCTCTGTAGTACTCTCG 63
Db 49 ATGGCTAGAAAGATGTTGGCTCCATGTTTCAGTGTGCTCTTTCATTGGAGCATTCGCT 108
QY 64 GCAATCCCGAGAGCGGTGGAAATCCATTGGGGTCTGCAATGGAATGGAACGGTGACAACCTC 123
Db 109 GCTGTCTCTACGAGTGTGAGTCCATCGGCGTATGCTACGGCGTGTATCGGCAACAACCTC 168
QY 124 CCCAGCCCGCGAGCTGTCTCACTCTAAGTCCCAACAACATAGTGGCATGGGACTC 183
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Db 229 TACTTGGCCGACGGGCGAGGCCCTCTCGGCGCTCCGCAACTCCGGCATCGGCTCATCTC 288
QY 244 GACGTCCCCCAACTCCGACCTCCAAAACAATTCCCTCCGACCAATCCGCGCCGACCAACTGG 303
Db 289 GACATCGGCAACGACAGCTGCGCCACATCGCCCGAGCACCTCCACGGCGGCTCTCTGG 348
QY 304 GTCCAAACCAACGTCGAAGCCTACCCAAAAGTTGGCTTCGATATCATCGCGTGGGAAC 363
Db 349 GTCCAGAAACAACGTGCGGCGCTTACTACCTCCGCTGAAACATCAAGTATCATCGCGCGGC 408
QY 364 GAAGTCATCCCGCGGCGGAGCTCAGTACGTCTCCAGCCATGAAACAATACAGTCC 423
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QY 424 GCGCTCTCTCTGCGCGCTTTCAGAAACATCAAGGTCTCCACATCAGTCTCTTGGCGTCC 483
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QY 484 GTCGTTACTCATATCCCGCTCAGCTGGCTCTTCTCTTCGATGATGCTCGACATG 543
Db 529 GTGGCCAACTCTCTTCGCGCGCTCGCGCGGCTGTTCAAGAACGCTATACGCGGACGTG 588
QY 544 GGTCCAAATCATACAGTTTCTAGCCAGCAATGGCTCCCGCATTTAGCCAAATCTACCC 603
Db 589 GCGCGGCTC-----CTGGCGAGCACCGCGCGCGCTGCTCGCCAAAGTCTACCC 639
QY 604 TACTTGAAGCTATGCTGGCAACTCCGGGATCCATCGACCTCTCATACGCGCTCTTTACTGCA 663
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Db 760 GTGACCGCGGTGACGCGGCGCTGGAGAACGCGCGCGCGGCGGTGAAGTGTGTTG 819
QY 781 TCGGAGAGTGTGCTGGCGCTCAGCGCGGCGGAGCAGCGCGAGCGGTCTTAATGCGCAGACT 840
Db 820 TCGGAGAGCGGTGGCGCTCGCGGGCGGTTTGGCGGTGCGCGGCAATGCGCGGAG 879
QY 841 TACAATTCGAATTTGATCAACCATGTGGGTGAGGGGACGCGGAGAGAGCGGAGCGGAT 900
Db 880 TACAACAGGGGCTGATCAACACAGTCTCGCGGCGGCGCACGCGCCAAAGAGCGGAGCGCTG 939
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Db 940 GAGACGTACATCTTCCCATGTTCAACGAGAACCCAGAACCGGGACGCCACGGAGAGG 999
Qy 961 AACTTTGGGCTGTTTACCTAACGAAACAGCCTGTCTATTTCGATCAGCTTC 1011
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US-08-812-025-11
; Sequence 11, Application US/08812025
; Patent No. 5804184
; GENERAL INFORMATION:
; APPLICANT: Transgenic pathogen-resistant organism
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Brumbaugh, Graves, Donohue and Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,025
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tenser, Arthur
; REGISTRATION NUMBER: 18,839
; NAME: Kole, Lisa
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Hordeum vulgare
; STRAIN: L.
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..48
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1050
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /codon start= 49
; OTHER INFORMATION: /function= "glucanase"
; OTHER INFORMATION: /product= "preprotein of the glucanase GluG"
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1051..1235
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /note= "14 nucleotides at the 3'end not shown."
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 1083..1088
; OTHER INFORMATION: /note= "potential polyadenylation"
; OTHER INFORMATION: signal
; NAME/KEY: polyA_signal

; LOCATION: 1210..1215
; OTHER INFORMATION: /note= "potential polyadenylation"
; OTHER INFORMATION: signal
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 133..1050
; US-08-812-025-11

Query Match 30.8%; Score 346.2; DB 2; Length 1235;
Best Local Similarity 60.4%; Pred. No. 2.1e-89;
Matches 611; Conservative 0; Mismatches 388; Indels 12; Gaps 2;
Qy 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCGATCGCATCCCTCTCTAGTACTCTCG 63
Db 49 ATGGCTAGAAAGATGTTCCCTCCCATGTTGAGTTGCTCTCTTCAATTGGAGCATTCGT 108
Qy 64 GCATCCCGAGAGGCGTGAATTCATATGGGGTCTCAATGGGAATGGACGGTGCACACCTC 123
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Db 169 CCTCCCGAGCGAGTGTGCGAGCTCTACAGGTCCAAAGGGCATCAACGGCATGGCATC 228
Qy 184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACCTCATCTC 243
Db 229 TACTTCGCGAGCGGCGAGGCCCTCTCGGCGCTCGCAACTCGGATCGGCTCATCTCCTC 288
Qy 244 GAGTCCCGCAACTCGGACCTCCAAACATTTGCTCCGACCAATCCGCGCCCACTCAACTGG 303
Db 289 GACATCGGCAACGACAGCTCGCCAAACATCGCGCGAGCACCTCCCAACGCGGCTCTCTG 348
Qy 304 GTCCAAACCAAGCTCCAGGCTTACCCAAACGTTGCTTCCGATACATCGCGTTCGGAAC 363
Db 349 GTCCAGAAACAGCTGCGGCCCTACTACCTCCCGTGAACATCAAGTATACATCGCCCGCGC 408
Qy 364 GAAGTCTATCCCGCGCGCAAGCTCAGTACGTCCTCCAGCCCATCAACAAATACAGTCC 423
Db 409 AACGAGGTGAGGCGGCGGCGCACGAGAGCATCTCGCGGCATCGGCAACCTCAACGGG 468
Qy 424 GCGTCTCTCTGCGCGCTTCAGAAACATCAAGGTCTCCACATCAGTCTCTCTCGGCGTCT 483
Db 469 GCGCTCTCGCGCGCGGCTCGGCGCATCAAGGTGTCCACTCCATCGGTTCCAGCAG 528
Qy 484 GTCGTACTCATATCCCCCTCAGTGGCTCTCTCTTCGATGATCTGTCGACATG 543
Db 529 GTGCCAACTCTTCCCGCGCTCCGCGCGGTGTTCAAGAACGCTATACGCGACGTG 588
Qy 544 GGTCAATCATACAGTTTCTAGCCAGCAATGGCTCCCGCTTACCTTTCGCAACATCTACCCC 603
Db 589 GCGCGGCTC-----CTGGCGAGCACCGCGCGCGCTGCTCGCCAAAGTCTACCCC 639
Qy 604 TACTTGAGTATGTGGCAACTCCGGATCCATCGACTCTCATAGCGCTCTTTACTGCA 663
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Db 940 GAGAGGTACATCTTCGCCATGTTCAACGAGAACCAAGAGACCGGGGACCGCCACGAGAGG 999
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RESULT 6

US-09-138-873A-11
; Sequence 11, Application US/09138873A
; Patent No. 6271438

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Transgenic pathogen-resistant organism

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Baker & Botts

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09138,873A

; FILING DATE: August 24, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Tenser, Arthur

; REGISTRATION NUMBER: 18,839

; NAME: Kole, Lisa

; REGISTRATION NUMBER: 35,225

; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 408-2500

; TELEFAX: (212) 765-2519

; TELEX: 238555

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1235 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Hordeum vulgare

; STRAIN: L.

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: 1..48

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 49..1050

; OTHER INFORMATION: /partial

; OTHER INFORMATION: /codon start= 49

; OTHER INFORMATION: /function= "glucanase"

; OTHER INFORMATION: /product= "preprotein of the glucanase GluG"

; FEATURE:

; NAME/KEY: 3'UTR

; LOCATION: 1051..1235

; OTHER INFORMATION: /partial

; OTHER INFORMATION: /note= "14 nucleotides at the 3'end not shown."

; FEATURE:

; NAME/KEY: polyA signal

; LOCATION: 1083..1088

; OTHER INFORMATION: /note= "potential polyadenylation signal"

; FEATURE:

; NAME/KEY: polyA signal

; LOCATION: 1210..1215

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OTHER INFORMATION: /note= "potential polyadenylation signal"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 133..1050
US-09-138-873A-11

Query Match 30.8%; Score 346.2; DB 3; Length 1235;

Best Local Similarity 60.4%; Pred. No. 2.1e-89;

Matches 611; Conservative 0; Mismatches 388; Indels 12; Gaps 2;

Qy 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCTTGTAGTACTCTCG 63
Db 49 ATGGCTAGAAAAGATGTTGCTCCATGTTTGCAGTTCCTCTCTTTCAITGGAGCATTCGCT 108
Qy 64 GCAATCCCGAGAGCGGTGGAATCCATTGGGGTCTGCAATGGAATGGAGCGGTGACAACCTC 123
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Db 289 GACATCGGCAACGACAGCTCGCCAAATCGCCGCCAGCACTCCAAACGGCGCTCTCTGG 348
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Qy 364 GAAGTCTATCCCGCGCGCAAGCTCAGTACGTCTCCAGCATGAAACAAACATACAGTCC 423
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Db 469 GCGCTCTCTCGCGCGGGGCTCGCGCCATCAAGGTGTCCACCTCCATCCGCTTGACGAG 528
Qy 484 GTCGGTACTCATATCCCGCTCAGTGGCTCTCTCTCCGATGCATCGTCGACATG 543
Db 529 GTGGCGAACTCTCCCGCGCTCGCGCGGTGTTCAGAACGCTACATGACGAGCGTG 588
Qy 544 GGTCCAAATCATACAGTTTCTAGCCAGCAATGGCTCCCGCATTTACCTTGCACATCTACCC 603
Db 589 GCGCGGCTC-----CTGGCGAGCACCGCGCGCGCTGCTCGCCAAAGTCTACCC 639
Qy 604 TACTTGAGCTATGCTGGCAACTCCGATCCATGACCTCTCATAGCGCTCTTTACTGCA 663
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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-105-390-5
Query Match 28.9%; Score 325; DB 3; Length 2169;
Best Local Similarity 62.1%; Pred. No. 3.7e-83;
Matches 587; Conservative 0; Mismatches 340; Indels 18; Gaps 4;

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Db 1291 AGCGACGTGTAAGCTCTACAAGTCCCAAGGGGATCGACTCCATCGCATCTACTTCCG 1350
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QY 253 AACTCCGACCTCAAAAACATTCCTCCGACCAATCCGCGCCACCAACCTGGGTCCAAACC 312
Db 1411 AACGAGACCTCGCGGTTCCGCGCGGACGACCGCGCGGTGCGGTGAGTCAAGCAG 1470
QY 313 AACGTCCAACTTACCCAAAGCTTTCGATCATCGCGCTCGGAAACGAAAGTATC 372
Db 1471 AACGTCCAGGCTTACCGGCGCTCTCTTCCGCTACATCGCGTCCGCAACGAGGTCA-- 1528
QY 373 CCGCGGCGCAGCTCAGTACGTCTCCAGCCATGACCAACATACAGTCCGCGCTCTCC 432
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QY 613 TATGCTGGCAACTCCGGATCCATGACCTCTCATACGCGCTCTTTACTGCACTCTGGTACA 672
Db 1759 TACGTGCGGCAACGAAAGACATAGCTCAACTACGCGCATGTTCCAGCGGGGACGAGC 1818
QY 673 GTCTGACAGGCGGTCTTACGCT---TACAAACAACTTTTCGATGCGCATGCTGACGCA 729
Db 1819 GTGACGAGCAGCGGCGGGGCTGATCTACAGAGGCTCTTTCGACGCGATGCTGATTC 1878
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RESULT 9

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US-09-105-390-41
; Sequence 41, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...921
; OTHER INFORMATION:
;
US-09-105-390-41
Query Match 28.4%; Score 319.6; DB 3; Length 921;
Best Local Similarity 62.2%; Pred. No. 8.5e-82;
Matches 578; Conservative 0; Mismatches 334; Indels 18; Gaps 4;
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QY 88 ATTGGGCTCTGCAATGGAATGACGGTGTGAACACTTCCCGCCGCGCGCGTGTCAAC 147
Db 1 ATTGGGCTGTGTACGGGTGTATGGCAACAACCTGCCGCGCGGAGCGAGCTGTGGAAG 60
QY 148 CTCTACAAAGTCCAAACAATAGTGTGCGATGCGACTCTACAGCCCGGACCAAGCAACTCTC 207
Db 61 CTCTACAAAGTCCAAAGGATGCACTTCCATGCGCATCTACTTCCGAGGAGCGACATCTCTC 120
QY 208 CAGGCGCTCTCAGGGCTCTAACAATCTATCTTCTCGAGCTTCCCAACTCCGACCTCCAA 267
Db 121 CAGGCACTCAGCGGCTCGAACAATCGCTTCCATGCGCATCTACTTCCGAGGAGCGACATCTCTC 180
QY 268 AACATTGCTCTCGAACAATCCGCGCCGACCAACTGGTGTCCAAACAAGTCAAGCTTAC 327
Db 181 GGTTCGCGCGGACGCGCCGCGGCTCGGCTCGGCTCAAGCAGACGTTCCAGGCTTAC 240
QY 328 CCAAAAGTGTGCTTCCGATACATCCGCGTGGGAAAGAGTCTATCCCGGGGCGCAAGT 387
Db 241 CCGGGGCTCTCTTCCGCTACATCCGCTGCGGCTGCGCAAGAGTCTA---CGGGGAGCAGAG 297
QY 388 CAGTACGCTCTCCAGGCAATGAACAATACATACAGTCCGCGCTTCTCTCTGCGGCTTCCAG 447
Db 298 GGCACATCTCTCCGCGCATGAAGAACCTCAACGCGCGCTCGGCGGCGCGGCTCGGC 357
QY 448 AACATCAAGTCTCCACATCAGTCTCTTCCGCGTCTGCTGCTATCTATATCCCGCTTCA 507
Db 358 GCGCTCGGGGTGTGACGCTCGGTGTCCAGGGGCGTATCGCCAACTCTCTACCGCGCTTCC 417
QY 508 GCTGCTCTCTCTCTTCCGATGATCGTCTGATGCTGCAATGCTGCAATCATACAGTTCTAGCC 567
Db 418 AACGGCTCTTCAACGAGA-----CTACATGTTTGATCATCTGGAGTACCTGGCG 468
QY 568 AGCAATGCTCTCCCAATTTCTGCAACATCTACCCCTACTTGGAGTCTGCTGGCAACTCC 627
Db 469 AGCAGCGGAGCGCGCTGCTGTGTAACTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTG 528
QY 628 GATCATGAGCTCTCTACGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 687
Db 529 AAAGACATCAGCTCTCAACTAGCCCACTTCCAGCGCGGCGAGCGGTCAGCGAGCGCGC 588
QY 688 TCCTACGCT---TACAACAACCTCTTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
Db 589 AGCGGCTGATCTACAGAGCTCTTCCAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648
QY 745 GAGAGCGCGGAGGCGGCAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804
Db 649 GAGAGCGCGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
QY 805 GCGGAGCAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
Db 709 GGTGGGTTTCGGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
QY 865 GTGGGTGAGGAGCGCGGAGGCGGCGG---GGCGATTGAGCTTACATATTTGCCATG 921
Db 769 GTCCAGGAGGACTTCCAGAGAGCAGGGGTGGGTTGGAGAGTACGTTGTTCGCCATG 828
QY 922 TTCAACGAGGATCAGAGCAGCGCGGCAAGGATTCAGAAATACTTGGGCTGTTTACCCCT 981
Db 829 TTCAACGAGAGACAGAGACCGGGGCTGAGACCGGAGGAGGCTTTCGGGCTGTTTCAACCCC 888
QY 982 AACGACAGCTGCTTATTCGATCAGCTTC 1011
Db 889 AACAGTCCGCTCTTACAAAATTAGATTTC 918

RESULT 10

US-09-105-390-51

; Sequence 51, Application US/09105390

; Patent No. 6288303

; GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond

; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

; TITLE OF INVENTION: and Genes

NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1008 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1008
OTHER INFORMATION:
US-09-105-390-51

Query Match 28.3%; Score 318.6; DB 3; Length 1008;

Best Local Similarity 60.4%; Pred. No. 1.7e-81;

Matches 585; Conservative 0; Mismatches 369; Indels 15; Gaps 3;

QY 46 CTCCTTGTAGTACTCTCGGCAATCCGAGAGCGGTGGAATCCATTGGGGTCTGCAATCGA 105

Db 49 CTTCTTGAGTTTATCTCAATCCCTGTAGCGGTGCAATCCGTGGTGTGTCTACGGC 108

QY 106 ATGACCGGTGACAACTCTCCCGCAGCGCGCGCGCGCTGCTCAACCTCTTACAAGTCCAAACAA 165

Db 109 ATGATCGGCAACGATCTCCCGTCGAAGAGCGAGCGTGTGAGCTCTACAATCCAAATGCGC 168

QY 166 ATAGCTGGCATGCGACTCTACAGCCCGGACCAAGCCACTCTCCAGGCGCTCAGGGCTCT 225

Db 169 ATCAAGACATGCGCATCTACTTCCCGGACGTCGAGGCGCATGAACGCGCTTGGCGGCA 228

QY 226 AACATCTACCTCACTCTCGAGCTCCCAACTCCGACCTCCAAAACATTTGCTCCGACCAA 285

Db 229 GGCATCGGCTCTATCTGCGGCTGCCAAGCATCTCTCATCTGACCTCGCGCGCAACCCG 288

QY 286 TCCGCGCGCACCACTGGGTCCAAACCAAGCTCCAAAGCTTACCCAAAGCTTGCCTTCCGA 345

Db 289 GCGTCCGCGCGCTCTGGGTGAGCGAGCGTCAAGCGCTTCCGTCGCGCGGTGAAACATC 348

QY 346 TACATCCGCTCGGAAAGCAAGTCAATCCCGCGCGGCGCAAGCTCAGTACGTCTCTCCAGCC 405

Db 349 AAGTACATCGCAGTCCGCAACAGAGATCTCCGCGGAGCGCCAGCGAGAAACATCTCTCCGCTC 408

QY 406 ATGAACACATACAGTCCGCGCTCTCTCTGCGCGGCTTCCAGACATCAAGTCTTCCACA 465

Db 409 ATGAGAAACATCAACGCGCGCTTGGCGCGGCGAGCATCACCGCGCTCAAGGCGTCCAGC 468

QY 466 TCAGTCTCTTCCGCGCTGCTGCGGTACCTCATATCCCGCTCAGCTGCTCTCTCTTCTTCC 525

Db 469 GCGTGAAGCTAGAGCTGTCACCAACAGCTTCGCGGCTCGCGGGTTC----- 522
Qy 526 GATGATCGTCGACATGGGTCGAATCATACAGTTCTPAGCAGCAATGGCTCCCAATTA 585
Db 523 ---GCGGCGCTTACATGACGGCGGTGCGCAAGCTCCTGCGATGACCGGGCGCGCGTG 579
Qy 586 CTTGCGCAACTACCTTACTTGAAGCTATGCTGGCACTCGGATCCATGCACTCTCA 645
Db 580 CTCGCCCAACTATACCTTCTTCCCTTACATCGCCCAACAGAGGACATCAGCTCTAAC 639
Qy 646 TACGCGCTTCTTACTGCACTCTGTTACAGTCTGACAGGAGGGTCTTAC---GCTTACAA 702
Db 640 TACGCGAGTTCAGGCGCGGACGAGCGGTGCGGCCGCCCAACACAGACTGTTGTAAGCC 699
Qy 703 AACCTCTTCGATGCCATGGTCGAGCAATTTGTAATTCGAGAGCGCGGAGGGCG 762
Db 700 AACCTGTTGAGCGCATGTCGACTCCGCTTACGCGCGCTGGACAAGCGCGCGCG 759
Qy 763 AATGTCCTGTTGTCGTCGAGAGTGGCTGCGCGCTGAGCGGGCGGACAGCGCGACG 822
Db 760 GCGCTGAGCATGTCGTCGAGAGCGGGTGGCGCTGCGCGCGCGGGGACTCGGCCACG 819
Qy 823 GTGTCATATGCGAGACTTACAAATTTGATCAACCATGTTGGTTCAGGGGACGCG 882
Db 820 ATCGACATCGCGCGGACTTACGTGAGAACCTGATTAGCATGCGAAGAGGGGACGCG 879
Qy 883 AAGAGCGCGGGCGGATTTAGACCTTACATATTTGCAATTTGATCAACGAGGATCAGAAGCAG 942
Db 880 AA---GCCGGGTGATCGAGACGTACGTGTTGCGCATGTTCAACGAGAACAGAGGCC 936
Qy 943 CGCAAGGGATGAGAAATTTGGGCTGTTTACCCCTAACGACAGCCGTCTATTTCG 1002
Db 937 GGGGAAGCCAGGAGCAAAATTTGGAGCCTTTACCCCTAACAGACAGAGTCTTACCCT 996
Qy 1003 ATCAGCTTC 1011
Db 997 ATCAATTC 1005

RESULT 11

US-09-105-390-2
; Sequence 2, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; TITLE OF INVENTION: and Genes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Petichory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1949 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-105-390-2
Query Match 27.6%; Score 310; DB 3; Length 1949;
Best Local Similarity 60.4%; Pred. No. 7.4e-79;
Matches 571; Conservative 0; Mismatches 360; Indels 15; Gaps 3;
Qy 75 AGCGTGGAAATCCATTGGGGTCTGCAATGGAATGAGCGGTGACAACTCCCCCAAGCGC 134
Db 1016 AGCGTGGAAATCCATTGGGGTCTGCAATGGAATGAGCGGTGACAACTCCCCCAAGCGC 1075
Qy 135 CGAGTGGTAACTCTTACAAAGTCCAAACAATAGCTGGGATGCGACTCTACAGCCCGA 194
Db 1076 CGAGTGGTAACTCTTACAAAGTCCAAACAATAGCTGGGATGCGACTCTACAGCCCGA 1135
Qy 195 CCAAGCCACTCTCCAGAGCCCTCCAGGGCTCTTAAATCTTACCTCATCTCCGACGTCCCAA 254
Db 1136 CGTGGAGCCCATGAAGCCCTTCGCGGCAAGGATCGGCTCATCTGTCGGCGTGGC 1195
Qy 255 CTCCGAGCTCCAAACATTTGCTCCGACCAATCCGCGCCCAACCAACTGGGTCCAAACCAA 314
Db 1196 CGACATCTCATGACCTCGCGCCCAACCCGCGCTCCGCGCTCGGGTTCGACGCGAA 1255
Qy 315 GGTCAAGCTTACCCAAAGCTTGGCTTCGATATATCGCGTTCGGAACGAGTCAATCCC 374
Db 1256 GGTCAAGCTTTCGTCGCGCGGTGAACATCAAGTATATCGCAGTCGCGCAACGAGATCTC 1315
Qy 375 CGCGGCGCAAGCTCAGTACGTCCTCCAGCCATCAACAAATACATCAGTCGCGCTCTCTC 434
Db 1316 CGCGGAGCCACGAGAACATCTCTCCGCTCATGCAACATCAACGCGCGCTTCGGCGC 1375
Qy 435 TGCGGCGCTTCAGAACATCAAGGTCTCCACATCAGTCTCTTCGCGCTTCGCGTACCTC 494
Db 1376 GCGGAGCATCACCGCGTCAAGGCGTCCACGGCGTGAAGCTAGACGCTCGTCAACACAC 1435
Qy 495 ATATCCCGCTCAGCTGGCTCTCTCTTCGATGCACTCGTTCGATTCGATTCGATTCAT 554
Db 1436 GTTCGCGCTTCGCGCGCGGTTC-----GCGCGCTTACATGACGCGCGTGGC 1486
Qy 555 ACAGTTTCTAGCAGCAATGGCTCCCAATTTGCAACATCTTACCTTACTGATCTGTTAGCTA 614
Db 1487 CAAGCTCTTGGATGACCGCGCGCGCTGCTCGCAACATCTACCTTACTTGGCTT 1546
Qy 615 TGCTGGCAACTCCGGATTCATCGACCTCTCATAGCCCTCTTTACTGATCTGTTAGCT 674
Db 1547 CATCGGCACAAAGAGGACATCAGCTCAACTAGCCAGTTCAGGCGCGGACGAGCT 1606
Qy 675 GGTACAGGACGGGTCTTAC---GCTTACAAACAACTCTTCGATGCGCATGTTGAGCTAT 731
Db 1607 GCGGACCCCAACACCGACTGGTGTACGCAACCTGTTTCGACGCGCATGTTGCTCGT 1666
Qy 732 GTACTCGCGCTCGAGAGCGCGCGGCGCGCAATGTCCTGTTGCTGTTGCTGAGAGTGG 791
Db 1667 CTACGCGCGCTGGACAGGCGCGCGCGCGCGGCGTCAAGATCTGTTGTTGAGAGGCGG 1726
Qy 792 CTGGCGCTGAGCGGCGGACAGCGGCGAGCGGTGTCTAATGCGCAGACTTCAATTC 851
Db 1727 GTGGCGCTGCGCGCGGGACTCGGCCACGATCGACATCGCGCGGACCTAGCTGACAG 1786
Qy 852 TTTGATCAACATGTTGGTTCAGGGGACCGCGAAGGCGCAGGGGCTTGGACCTACAT 911
Db 1787 CCTGATTAAGCATGCGAAGAGGGGACCGCGAA---GCCGGGGGTGATCGAGACGATCGT 1843
Qy 912 ATTTGCCATGTTCAACGAGGATCAGAGCAGCGCGCAAGGGATTTGAGATAATCTTTGGCT 971

Db 1844 GTTCGCCATGTTCAACGAGAACAGACAGAGCCCGGGAGAGCCAGGAGCAAAACTTTGGAGC 1903
Qy 972 GTTTTACCTTAACGACAGCCGTGTCTATTTCGATCAGCTTTCACTTGA 1017
Db 1904 CTTTACCTTAACAGACAGCAGTCTTACCTTATCAATTTCCAGTGA 1949

RESULT 12

US-09-105-390-35
; Sequence 35, Application US/09105390
; Patent No. 6288303

GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

; TITLE OF INVENTION: and Genes

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/105,390

; FILING DATE: Filed herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/050,675

; FILING DATE: 25-JUN-97

; ATTORNEY/AGENT INFORMATION:

; NAME: Pettichory, Joanne R.

; REGISTRATION NUMBER: P42,995

; REFERENCE/DOCKET NUMBER: 2000-0455,30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-324-0880

; TELEFAX: 650-324-0960

; TELEX:

; INFORMATION FOR SEQ ID NO: 35:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 918 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 1..918

; OTHER INFORMATION:

US-09-105-390-35

Query Match 26.5%; Score 298; DB 3; Length 918;
Best Local Similarity 60.0%; Pred. No. 1.4e-75;
Matches 556; Conservative 0; Mismatches 355; Indels 15; Gaps 3;

Qy 89 TTGGGCTGCAATGGAATGACGGTGACAACTCCCGCCGACCGCGACGTCGTCAACC 148
Db 2 TTGGTGTGTGTAGCGCATGATCGGCAACGATCTCCCGTCGAAGAGCGACGTCGTGCAGC 61
Qy 149 TCTACAGTCCCAACACAGTACGTCGCGACGATCTACAGCGCCGACCAAGCCACTCTCC 208
Db 62 TCTCAAAATCAATGGCATCAAGACATGCGCATCTACTTCCGCGAGCGTCGAGGCCATGA 121
Qy 209 AGGCGCTCCAGGCTCTAACTACCTCATCTCGAGCTCCCAACTCCGACCTCCAAA 268
Db 122 ACGCCTCGCGGACACAGGCAATCGGCTCATGTCGGGTGCGCAACGACATCTCTATCG 181
Qy 269 ACATTGCTCCGACCAATCCCGCCGACCAACTGGGTCCAAACCAAGCTCCAGCCTACC 328

Db 182 ACCTCGCGCCCAACCCGGCGTCCGCGCGTCTCTGGTTCGACGCGAAACGTTCAAGCCGTTCC 241
Qy 329 CAACAGCTTGGCTTCCGATACATCGCGCTCGGAAACGAAGTCTATCCCGCGCGCAAGCTC 388
Db 242 TCCCGCGGTGAACATCAAGTACATCGCAGTCGCGAACGAGATCTCCGCGGAGCCACGC 301
Qy 389 AGTACGTCTCCAGCCATGAACAACATACAGTCCGCGCTCTCTCTGCGCGCTTTAGA 448
Db 302 AGAACATCTCCCGGTCTATCGAAGAACATCAACGCGCCCTCGCGCGGAGCATCAACCG 361
Qy 449 ACATCAAGGTCTCCACATCAGTCTCTCTCGGGGTGTCGTGACCTCATATCCCGCTCAG 508
Db 362 CGCTCAGGCGGTCCACGCGGTGAAGCTAGACGTCGTCAACCAACAGCTTCCCGCGCTCG 421
Qy 509 CTGGGTCTCTCTTCCGATGATCGTCGACATCGGTCCTCAATCATACAGTTTCTAGCCA 568
Db 422 CGGGGTGTTT-----GGGGCGCTTACATGACGCGCGTGGCGAAGCTCTCTGCGAT 472
Qy 569 GCAATGGCTCCCCATTACTTTCGCAACATCTACCCCTACTTTCGAGCTATGTCGCAACTCG 628
Db 473 GCACCGCGCGCGCGCTGCTCGCAACATCTACCCCTACTTTCGCTTACATCGGCAACAGA 532
Qy 629 GATCATGACCTCTCATACGCGCTCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688
Db 533 AGGACATCAGCTCAACTACGCTTCAGGCGCGGACGACGCTGCGCCGCAACCA 592
Qy 689 CCTAC---GCTTACAAACACCTCTTCGATGCCATGCTGCGAGCTGCTGCTGCTGCTGCTGCT 745
Db 593 CGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 652
Qy 746 AGAGCGCGGAGGCGCGAATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 805
Db 653 ACAAGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Qy 806 CGCGGACAGCGCGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 865
Db 713 CGCGGACCTCGGCGCACGATCGACATCGCGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 772
Qy 866 TGGGTCAAGGCGGACCGCGGAGGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 925
Db 773 CGAAGAGGCGGACCGCGAA---GCCGGGGGTGATGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
Qy 926 ACAGGATCAGAGCAGCGCGCAAGGATTGAGAACTTTGGGCTGTTTACCCCTAACG 985
Db 830 ACAGAGACCAAGCGCGGAGCCAGCGAGCAAACTTTGGAGCTTCTACCCCTAAC 889
Qy 986 AACAGCTGCTTATTCGATCAGCTTC 1011
Db 890 AGACAGCAGTCTACCTATCAATTC 915

RESULT 13

US-09-105-390-53
; Sequence 53, Application US/09105390
; Patent No. 6288303

GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

; TITLE OF INVENTION: and Genes

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Pettithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 996 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...996
; OTHER INFORMATION:
;
US-09-105-390-53

Query Match 26.2%; Score 295.2; DB 3; Length 996;
Best Local Similarity 59.2%; Pred. No. 9.6e-75;
Matches 586; Conservative 0; Mismatches 383; Indels 21; Gaps 4;

QY 25 TCCATTGGGCTGCAGTGCATCCCTCTTGTAGTACTCTCGCAATCCCGAGAGGGGTGAA 84
DB 25 TCTATGTTCAATTTGCTCTGATCATTTGGAGATTGTTCTTGTCTCAACAACTGTGAA 84
QY 85 TCCATTGGGCTGCAGTGCATCCCTCTTGTAGTACTCTCGCAATCCCGAGAGGGGTGAA 144
DB 85 TCCATTGGGCTGCAGTGCATCCCTCTTGTAGTACTCTCGCAATCCCGAGAGGGGTGAA 144
QY 145 AACCTCTAAGTCCAAACAATAGTGGCATGAGTCTACAGCCCGGACCAAGCCACT 204
DB 145 CAGCTGTACAAGTCCAAAGGATCAACGGCATGGCATCTACTACCCCGACAAAGAGGCG 204
QY 205 CTCAGGCGCTCCAGGCTCTAATCTTACCTCTCTCGAGTCCCACTCCGACCTC 264
DB 205 CTCAGGCGCTCCAGGCTCTAATCTTACCTCTCTCGAGTCCCACTCCGACCTC 264
QY 265 CAAACATTTGCTCCGACCAATCCCGCGCCACCACTGGGTCCAAACCAAGTCCAGCC 324
DB 265 AACCTCGCGGCTCTCTCCAGCGCGCGGTGGGTCCGGGACAAAGTCAAGCCCTAC 324
QY 325 TACCCAAAGTGTCTTCGATACATCGCGGTGGGAAAGCAAGTCAATCCCGGGGCGAA 384
DB 325 TACCCGGCGCTCAACATCAAGTACATCGCGGTGGGAAAGCAAGTCAATCCCGGGGCG 381
QY 385 GCTCAGTACGCTCTCCAGGATCAACATACAGTCCGCGCTCTCTCTCTCGCGCTT 444
DB 382 ACAGTACGCTCTCTCCAGGATCAACATACAGTCCGCGCTCTCTCTCTCGCGCTT 441
QY 445 CAGAACATCAAGTCTCCAGGATCAACATACAGTCCGCGCTCTCTCTCTCGCGCTT 504
DB 442 GGGCGCATCAAGGCTCCAGGATCAACATACAGTCCGCGCTCTCTCTCTCGCGCTT 501
QY 505 TCAGTGTGCTCTCTCTTCGATGCAATGCTGCAATTTGGGTCCCAATCATACAGTTCTA 564
DB 502 TCCGCGCGGTCTTCAGGAGCGCTTACATGAGGACATCGCGCTCTCTCTCTCGCGCTT 552
QY 565 GCCAGCATGCTCCCAATTACTTCCGACATCTACCCCTACTTGGATGCTGGCAAC 624
DB 553 ---TGACCGCGCGCGCTGCTGCTCCCAAGTGTACCGCTTCTGCGCTTCTGCGCGGAA 609
QY 625 TCCGATCCATGAGCTCTCTACAGCGCTCTTCTTCTGATCTGCTGATGCTGCTGCTG 681
DB 610 CCGCGGACATCAGCTCTCAATACGCGGCTTCCGCGCGGCGGACCAAGTGGAGGCCA 669
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QY 682 GACGGTCTTACGCTTACAAACCTCTTGCATGCCATGTCGACGCAATGTTACTCGGCC 741
DB 670 AACAAACGGGCTACCTTACACCACTGTTCGACCCCATGATGGACCGCGTGTACGCCG 729
QY 742 CTGAGAGCGCGGAGGGCGCAATGTCCCTTGTTCGTGTCGAGAGTGGCTGGCCGCTCA 801
DB 730 CTGGAAGAAGCGCGCGCGGGAACGTGAGGGTGTGTGTCGAGAGGGGTGGCCGCTG 789
QY 802 GCGGCGGAGACAGCGCGGACGCTCTTAATGCGCAGACTTACAATTCGAATTTGATCAAC 861
DB 790 GCGGAGGGTTCGGGGCGGAGCGTGCACAATGCGAGGCGGTACAACACGAGGCTGATCGAC 849
QY 862 CATGTGGGTGAGGAGCGCGGAGAGCGGCGGATTCGAGACCTACATATTTGCCATG 921
DB 850 CATGTGGT---GGCACGCCCAAGAGCGCGGCACTGGAGGCGTACATATTCGCCATG 906
QY 922 TTCAACGAGGATCAGAAGCAGCGCCGCAAGGGATTCAGAAATTAACCTTTGGGCTGTTTACCCT 981
DB 907 TTCAATGGAACACAGAGAGACGGGATCCCAACCGAGAGAACTTTGGGCTCTTCTACCT 966
QY 982 AACGAACAGCTGTCTATTTCGATCAGCTTC 1011
DB 967 AACAAAGTCCGCGGTGTATCCCATCCGGTTC 996
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RESULT 14
US-09-105-390-3
; Sequence 3, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; TITLE OF INVENTION: and Genes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Pettithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-105-390-3
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Query Match 25.5%; Score 286.8; DB 3; Length 2317;
Best Local Similarity 59.8%; Pred. No. 4e-72;
Matches 562; Conservative 0; Mismatches 357; Indels 21; Gaps 4;
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75 AGCGCTGGAATCATTTGGGCTTGCAATGGAATGACGGTGAACATCTCCCGACCCGC 134
1393 AGCTGTGCAATCATCGGGGTGTGCTATGGCTTCTCGGCAACACCTCCCGTCGGGAG 1452
135 CGAGCTGCTCAACCTCTCAAGTCCAAACATAGTGGCTGCGATCTTACAGCCCGA 194
1453 CGAGGTGGTCAAGCTGTACAGTCCAAAGGCTCAACGGCATCGGCATCTACTACCCGA 1512
195 CCAAGCCACTCTCCAGGCTCCAGGGCTTAACTATCTACCTCATCTCGAGTCCCAA 254
1513 CAAGAGGGCTCAAGCCCTCGGCACTCCGGTATCGCCCTCATCTCGAGTGGCGA 1572
255 CTCGCACTCTCAAAACATTTGCTCCGACCAATCCGCGCCACCAATGGGTCCAAACCAA 314
1573 CCAAGTGTCAACCTCGCGCCAGCTCTCCAAAGCGCGCGGTGGGTCCGCGACAGT 1632
315 CGTCAAGCTCAACCAAGTGTGCTTCGATACATCGCGCTGGAAGCAAGTATCC 374
1633 CAGGGCTTACTACCGCGCGCTCAACATCAAGTACATCGCGCTCGCAACGAGG---TGA 1689
375 CGCGCGCCAAAGTCTAGTCTCTCCAGCCATGAACACATACAGTCCGCCCTCTCTC 434
1690 AGCGCGCCACAGTAGATCTCTCGGCCATCCGCAAGTCACTCCGCCCTGGGCTC 1749
435 TCGCGGCTTCAGAAACATCAAGTCTCTCCATCACTCTCTTCGGCGGTGTCGGTACCTC 494
1750 GGTGCGCTTCGGCGCATCAAGCGCTCCACCGCGGTGAAGTTCGAGCATCTCCAACTC 1809
495 ATATCCCGCTCAGTGGCTCTCTCTTCGATGATGCTGCAATTTGGGTCCAAATCAT 554
1810 CTACCCAGCTTCGGCGGTCTTCAGGAGCCCTACATGAAGGACATCGCGGTACCG 1869
555 ACAGTTTCTAGCCAGTGGCTCCCATTTCTGCGCACTACCTACCTACCTACTTACGTA 614
1870 AT-----GCACCGCGCGCGCTGCTCGCCAAAGGTACCGGTACTTCCGCTA 1917
615 TGCTGGCAATCTCGGATCATGCACTCTCATACCGCTCTTTACTGATCTGTGACAGT 674
1918 CAGGGGGAACCGCGGACATCAGCTCACTACGCGAGTTCGCGCGGCGGACACAGT 1977
675 ---CTACAGGAGCGGTCTACGTTTACAAACCTCTTCGATGCAATGGTGGACGATT 731
1978 GAGGAGCCAAACAAACGGGCTCACCTACACCAACCTGTTCGACGCGCATGATGACGCGT 2037
732 GTACTCGGCTGGAGAGCGCGGAGCGCGGATGCTCTCTGCTGCTGCTGCGAGTGG 791
2038 GTACCGCGCTGGAGAGCGCGCGCGCGCGGAAAGTGAAGGTGGTGTGGAGAGCGG 2097
792 CTGGCGCTCAGCGCGCGGACAGCGCGGAGCGGTGTCTAATGCGCAGACTTACAAATCCAA 851
2098 GTGGCGCTCGGCGGAGGTTTCGGGCGAGCGGTGCAATGCGAGGCGTACACCGGG 2157
852 TTGTATCAACATGTTGGTTCAGGGGACCGCGGAGAGGCGAGGGCGATTGAGACCTACAT 911
2158 GCTGATCACCATGTGCT---GGCAGCCCAAGAGCGCGCGGCACTGGAGGCGTACAT 2214
912 ATTTCTATGTTCAAGAGGATCAGAGCGCGGCAAGGATTTGAGATTAATTTGGGCT 971
2215 ATTCCCATGTTCAATGAGAACCAAGAGAGGAGATCCCAAGAGAGAAATTTGGGCT 2274
972 GTTTTACCTTAACGAACGCTGTCTATTTCGATCAGCTTC 1011
2275 CTTTACCTTAACAGTCCCGGTGTATCCATCCGGTTC 2314

RESULT 15

US-09-105-390-37

; Sequence 37, Application US/09105390

; Patent No. 6288303

; GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond

; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..909
OTHER INFORMATION:
US-09-105-390-37

Query Match 24.8%; Score 278.6; DB 3; Length 909;
Best Local Similarity 59.5%; Pred. No. 5.6e-70;
Matches 552; Conservative 0; Mismatches 354; Indels 21; Gaps 4;

Qy 88 ATTGGGTCTGCATATGGAATGGAAGTGGTGAACCTCTCCCGACGCGCGCGAGCGTCTGTCAC 147
Db 1 ATCGCGGTGTCTATGGGTTCTCGGCAACAACTCTCCGTCGCGGAGCGAGTGGTGCAG 60
Qy 148 CTCTACAGTCCAAACACATAGCTGGCATGCGATCTTACAGCCCGCGACCAAGCCACTCTC 207
Db 61 CTGTACAGTCCAAAGGATCAACGCGCATCAACGCGATGCGCATCTACTACCCCGCAAGAGGCGCTC 120
Qy 208 CAGCGCTCTCAGGCGCTTAAACATCTACCTCATCTCTCGACGTCCTCCCACTCCGACCTCAA 267
Db 121 AACGCGCTCGCACTCGGTATCGCCTCATCTCGACGTCGGGACCAAGTGTGTCAC 180
Qy 268 AACATGCTCTCGGACCAATCGCGCCACCACTGGGTCCAAACCAAGCTCCAGCTCCAGCTAC 327
Db 181 CTCGCGCGCAGCTCTCTCAAGCGCGCGGTGGGTTCGCGACCAAGCTCAGGCGCTTACTAC 240
Qy 328 CCAAGCGTTCGCTTCGATATACATCGCGTTCGGAACGAGTATCCCCGCGGCGCCAGCT 387
Db 241 CCGCGCGTCAACATCAAGTATACATCGCGTTCGCAACGAGG---TGAAGGCGCGCGCCACG 297
Qy 388 CAGTACGCTCTCCAGCGCATGAACAAACATACAGTCCGCGCTCTCTCTGCGCGGCTTCAG 447
Db 298 AGTAGCATCTCTCCCGGCGATCCGCAACGTCATCTCCGCGCTGGGCTCGGTTCGGCTCGGG 357
Qy 448 AACATCAAGGTCTCCACATCAGTCTCTCTCGGCGTTCGCTGCTGCTATATATCCCCCTCA 507
Db 358 CGCATCAAGGCGTCCACCGGCGTGAAGTTTCGACGTCATCTCCAACTCTCTCAACCTCTCCACCCCTCC 417

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Qy 508 GCTGGGTCCTTCTCTTCCGATGATCGTCGACATTTGGGTCCAATCATACAGTTTCTAGCC 567
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Qy 418 GCCGGGTCTTCAGGAGCGCTACATGAAGGACATCGCGCGTACCGAT----- 466
Db      |||
Qy 568 AGCAATGGCTCCCAATTACTTGCCAAATCTACCCCTACTTTGAGCTATGCTGGCAACTCC 627
Db      |||
Qy 467 -GCACCGCGCGCGCTGCTCGCCAACTGTACCGTACTTCGCTACAGGGGGAACCCG 525
Db      |||
Qy 628 GGATCCATCGACCTCTCATAGCCCTCTTTACTGCATCTGGTACAGT---CGTACAGGAC 684
Db      |||
Qy 526 CGGACATCAGCCCTCAACTAGCCACAGTTCGCGCGGGGCAACCGGTGAGGGACCCAAAC 585
Db      |||
Qy 685 GGGTCCTACGGTTTAAACAACTCTTCGATGCCATGGTCGACGCAATTGTACTCGGCCCTG 744
Db      |||
Qy 586 AACGGGCTCACTACACCAACTGTTCGACGCCATGATGGACGCGTGTACGCCGCGCTG 645
Db      |||
Qy 745 GAGAGCGCCGAGGGCCGAATGTCCCTGTTGTCGAGAGTGGCTGGCCCGTCAGCG 804
Db      |||
Qy 646 GAGAAAGCCGCGCGCGGAACTGTAGGGTGTGGTGTGCGAGAGCGGGTGGCGCTCGGCG 705
Db      |||
Qy 805 GCGGGACAGCGGCGACGGTGTCTAATCGGCAGACTTACAATTCCAATTTGATCAACCAT 864
Db      |||
Qy 706 GGAGGGTTCGGGGGAGCGTGGACAATCGAGGGCGTACAACACAGGGGCTGATCGACCAT 765
Db      |||
Qy 865 GTGGGTCAAGGGACCGCGAAGAGGCCAGGGCGATTGAGACTACATATTTGCCATGTTTC 924
Db      |||
Qy 766 GTGCGT---GGACGCCCAAGAGGCGCGGGCACTGGAGGGGTACATATTCGCCATGTTTC 822
Db      |||
Qy 925 AACGAGGATCAGAAGCAGCCGCGAGGGGATTCAGAGATTAACTTTGGGCTGTTTTACCCCTAAC 984
Db      |||
Qy 823 AATGAGAACCAAGAGAACGGGGATCCACCGAGAGAACTTTGGGCTCTTCTACCCCTAAC 882
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Qy 985 GAACAGCCTGTCTATTGATCAGCTTC 1011
Db      |||
Qy 883 AAGTCGCCCGTGTATCCCATCGGTTTC 909
Db      |||
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Search completed: April 7, 2006, 22:17:24
Job time : 247 sec.


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QY 361 AACGAAGTCATCCCGCGGCGCAAGCTCAGTACGTCCTCCAGCCATGAACAACATACAG 420
Db 361 AACGAAGTCATCCCGCGGCGCAAGCTCAGTACGTCCTCCAGCCATGAACAACATACAG 420
QY 421 TCCGCCCTCTCCTCTGCGGCGCTTCAGAACATCAAGGTCTCCACATCAGTCTCTTCGGC 480
Db 421 TCCGCCCTCTCCTCTGCGGCGCTTCAGAACATCAAGGTCTCCACATCAGTCTCTTCGGC 480
QY 481 GTCGTGGTACCTCATATATCCGCCCTCAGTGGTCTCTCTCTTCGATGCAATGCTGCA 540
Db 481 GTCGTGGTACCTCATATATCCGCCCTCAGTGGTCTCTCTCTTCGATGCAATGCTGCA 540
QY 541 TTGGGTCCAAATCATACAGTTTCTAGCAGCAATGCTCCCAATTAATCTTGGCAACATCTAC 600
Db 541 TTGGGTCCAAATCATACAGTTTCTAGCAGCAATGCTCCCAATTAATCTTGGCAACATCTAC 600
QY 601 CCCTAATTTGAGTATGCTGGCAACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACT 660
Db 601 CCCTAATTTGAGTATGCTGGCAACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACT 660
QY 661 GCATCTGGTACGTGCTACAGACGGGTCTTACGGTTTAAACAACCTCTTGAATGCCATG 720
Db 661 GCATCTGGTACGTGCTACAGACGGGTCTTACGGTTTAAACAACCTCTTGAATGCCATG 720
QY 721 GTCGACGCAATGTACTTCGGCCCTGAGAGCGCGGAGCGGAGCGGAGTGTCTGTGTGCTG 780
Db 721 GTCGACGCAATGTACTTCGGCCCTGAGAGCGCGGAGCGGAGCGGAGTGTCTGTGTGCTG 780
QY 781 TCGGAGAGTGGTGGCCGCTCAGCGGCGGAGCAGCGGAGCGGAGTGTCTTAATGCGCAGACT 840
Db 781 TCGGAGAGTGGTGGCCGCTCAGCGGCGGAGCAGCGGAGCGGAGTGTCTTAATGCGCAGACT 840
QY 841 TACAATTTCAATTTGATCAACATGTGGGTCAAGGAGCGCGGAGCGGAGCGGAGTGTCTTAAT 900
Db 841 TACAATTTCAATTTGATCAACATGTGGGTCAAGGAGCGCGGAGCGGAGCGGAGTGTCTTAAT 900
QY 901 GAGACCTACATATTTGCCATGTTCAACAGGATCAGAGCGGAGCGGAGCGGAGTGTCTTAAT 960
Db 901 GAGACCTACATATTTGCCATGTTCAACAGGATCAGAGCGGAGCGGAGCGGAGTGTCTTAAT 960
QY 961 AACTTTGGGCTGTTTACCTTAACAGGATCAGAGCGGAGCGGAGCGGAGTGTCTTAAT 1020
Db 961 AACTTTGGGCTGTTTACCTTAACAGGATCAGAGCGGAGCGGAGCGGAGTGTCTTAAT 1020
QY 1021 ATTGATCAGATGAATATAAATAAAGTCTTATATTGTAAGGCAAGCTCGTAATTGA 1080
Db 1021 ATTGATCAGATGAATATAAATAAAGTCTTATATTGTAAGGCAAGCTCGTAATTGA 1080
QY 1081 TAGCCATCTAGTAATATAGCTCCGCTTAATTAATACTATAAATA 1125
Db 1081 TAGCCATCTAGTAATATAGCTCCGCTTAATTAATACTATAAATA 1125

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RESULT 2

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US-10-437-963-64217
; Sequence 64217, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

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; SEQ ID NO 64217
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65383C.1
US-10-437-963-64217

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Query Match 38.3%; Score 431.4; DB 7; Length 1333;
Best Local Similarity 66.8%; Pred. No. 3.8e-124;
Matches 682; Conservative 0; Mismatches 321; Indels 18; Gaps 4;

QY 4 ATGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCTCTGTAGTACTCTCG 63
Db 112 ATGCAAAAGCATGGGTGCTTCCGTTTAACATGGCATGGTGGTGGAG---TTGGG 168
QY 64 GCAATCCCGAGAGCGGTGGAATCATTTGGGTCTGCAATGGAATGGAGCGGTGAACAACCTC 123
Db 169 GCCATTCTACAGTGGTGCATCTATCGCGGTGTGTACGGCGTGTATCGGGAACAACCTG 228
QY 124 CCCAGCGCGCGAGCGTGTCAACTCTACAAGTCCACAACATAGCTGGGATGGGACTC 183
Db 229 CCGTCGCGAGCGAGCTGTGCAGCTCTACAAGTCCACAACCGCATCGATCTCATGCGCATC 288
QY 184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAACATCTACATCTCATCTC 243
Db 289 TACTTCCCAAGAAGCGACATCTCTCAGGCCCTCAGCGGCTCAAGCATCGCCCTCACCATG 348
QY 244 GACGTCCCAACTCCGACCTCCAAAATGTCCTCCGACCAATCCGCGCGCACCAACTGG 303
Db 349 GACGTCCGCAACGATCAGCTCGGCTCTCCGCTCCGACCCCTCCGCGCGCGCGCTTC 408
QY 304 GTCCAAACCAACGTCGAAGCTTACCCAAAGTTCGATACATCCGATACATCCGCGTGGAAAC 363
Db 409 GTCCAGAACAACTCCAGGGGTTCGCGGGCGTCAACTTCCGCTACATCACCGTGGCAAC 468
QY 364 GAACTCATCCCGCGCGCAAGCTCAGTACGTCCTCCAGCGCATGAACAACATACAGTCC 423
Db 469 GAGG---TTTCCGCGGGGACACCGAGAAATCTCTCCGCGCATGCGAGNAATGAGAACAGC 525
QY 424 GCCCTCTCTCTGCGGCGCTTCAGAAACATCAAGGTCTCACATCAGTCTCTCTCGGCGTC 483
Db 526 GCCCTCTCGCGCGCGCTCGGCAACATCAAGGTGTGACGTGCGTGTCTCCAGGGCGTG 585
QY 484 GTCGTGACCTCATATCCCCCTCAGCTGGCTCTCTCTCTTCGATGCAATCGTCGACATG 543
Db 586 ACCG---CCGGCTTCCGCGCGTCCGCGGCACTTCTCCGCG---TCGCACTG 633
QY 544 GGTCCAAATCATACAGTTTCTAGCCAGCAATGGCTCCCAATTAATTTGCCAAATCTTACCCC 603
Db 634 GGGCCCATAGCTCAGTACCTGCGAGCACCGCGCGGCGGCTGTCTCGCNAAGTCTTACCCC 693
QY 604 TACTTGAGCTATGCTGGCAACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACTGCA 663
Db 694 TACTTGGCTTACGTGGGCAACAGCGCCAGATCGACATCAACTACGCGCTCTTTCACGTCG 753
QY 664 TCTGTACAGTCTGTCAGGAGGGGTCTTACGCTTACAGAACACCTCTTCGATGGCATGTC 723
Db 754 CCGGCGACGGTGGTGCAGGACCGGCGGCAACCGCTACCAAGAACCTGTTCGACGCCATCGTC 813
QY 724 GACGATTTGACTCGGCGCTCGAGAGCGCGGAGGGCGGAATGTCCCTGTGTGTGTGTGTCG 783
Db 814 GACAGTTTCTACTCGCGCTGGAGAGCGCGCGCGGCGGAGCGTCCCGATCGTGTGTGTCG 873
QY 784 GAGAGTGGCTGGCGCTCAGCGGCGGGGACAGCGCGGAGCGGTGTCTTAATGCGCAGACTTAC 843
Db 874 GAGAGCGGGTGGCGCTCGGCGCGGCGACGCGCGGAGCGCGGCAACCGCGCAGACGCTAC 933
QY 844 AATTCCAAATTTGATCAACCATGTGGTTCAGGGGAGCGCGAGAGCCAGGGCGGATGAG 903
Db 934 AACCAGAACCTGATCAACACGTCGGGCGAGGGGACGCCCAAGAGGCCCGGGGAGCATCGAG 993
QY 904 ACCTACATATTTTGCATGTTTCAACAGGATCAGAAGCAGCGCGCAAGGATTTGAGAAATAAC 963

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Db 994 ACCATCAATTTGCGCATGTTCAACGAGAACCCAGAGGGGAGGCGACGAGAGGCGCAC 1053
Qy 964 TTGGGCTGTTTACCTTAACGAAACAGCCTGTCTATTTCGATCAGCTTTCATTTGAGAAAT 1023
Db 1054 TTGGGCTCTTCAACCGGAGCAGTCCGCGCATCTCCATCAATTTCTAAGAAATGTT 1113
Qy 1024 T 1024
Db 1114 T 1114

RESULT 3
US-10-739-930-5127
; Sequence 5127, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; ; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 5127
; LENGTH: 1439
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1439)
; OTHER INFORMATION: unsure at all n locations
; ;
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER579_3
US-10-739-930-5127

Query Match 38.0%; Score 427.2; DB 8; Length 1439;
Best Local Similarity 66.0%; Pred. No. 8.4e-123;
Matches 656; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

Qy 21 CATCTCCATGGTGCATGGCATCCCTCTGTGTAGTACTCTCGGCAATCCGAGAGGGGT 80
Db 96 CATGTTTTCGGTGGCGTGTGGCCCTCTTGTGGAGTGTCTTGGGATCCATTCTCTGACGGGT 155
Qy 81 GGAATCCATTGGGGTCTGCAATGGAATGAGCGGTGACAACTCCCGCAGCGCGCGAGGT 140
Db 156 GCAGTCCATCGCGGTGTCTAGCGGTGACGCGCGCGCTGCGCTCGCGCAGGAAAT 215
Qy 141 CGTCAACCTCTACAAAGTCCAAACATAGCTGGCATGGACTCTACAGCCCCGACCAAGC 200
Db 216 CGTGCACTTACCAAGTCCAAAGGATCACCGGCATGCGCATCTACTTCCCGGAGCGCA 275
Qy 201 CACTTCAGGCGCTTCAGGGCTTAAACATCTACCTCATCTCTGACGTGCCCACTCCGA 260
Db 276 CGCCCTCAGGCGCTTCAGGCGGAGCAACATCGACCTCATCTCATCGACGTGGCGCAACGGA 335
Qy 261 CCTCAAAACATTTGCTCCGACCAATCCGCGCCACCACTGGGTCCAAACCAAGTCCA 320
Db 336 CTTGCTCTCTCTCGCTCCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 395
Qy 321 AGCTTACCAAAAGTGTGCTTCCGATACATCGCGCTCGGAAACGAAGT---CATCCCCGG 377
Db 396 GCGCCACCAAGGCTCAACATCAAGTATCATCGCGCGCGCGCGCGCGCGCGCGCGCGCG 455
Qy 378 CGGCGCAAGCTCAGTACGTCTCTCCAGCATGAAACAAATACAGTCCGCGCTCTCTCTGCG 437
Db 456 CGGCGACACGGGGAACATCTCTCCGCGCATGAGAACTCGAGCGCGCACTCTCTCGCGCG 515
Qy 438 CGGCGCTCAGAACATCAAGGTCTCCACATCATCTCTCTCGCGCTGCTGCTGCTGCTGCT 497
Db 516 CGGCGTAGCGGCGCATCAAGGTGTCCACGTGCGGTGTGCGAGGGCGGTGACCGCGGCTACC 575
Qy 498 TCCCCCTCAGTGGCT 557

Db 576 TCCCTCCCAAGGACCTTCTCTCGCGGCTTACA-----TGGGACCCCATCGCGCA 623
Qy 558 GTTTCAGCGCAATGCTCCCAATTACTTGGCGAACATCTTACCCCTACTTGAAGTATGC 617
Db 624 GTACTTGGCGACCAACCGCGCGCGCTGCTCGCCAAACGTTTACCCCTACTTCTCGTACGT 683
Qy 618 TGGCAACTCCGATCCATCGACCTCTCATACGCGCTCTTTTACTGATCTTGGTACAGTCTGT 677
Db 684 GGACAAACAGGCCAGATCGACATCAACTACGGCTCTTCACTGCGCGGCAACCGTGT 743
Qy 678 ACAGAACGGGTCTTACGTTTACAAACACTCTTTCGATGCACTGGTGCAGCAATTTGATCTC 737
Db 744 GCAGGACGCGCGCAACCGGTACCAAGAACTGTTCGAGCGCTCGTCGACACGCTTCTACTC 803
Qy 738 GGCCTCGAGGCGCGCGGAGGCGCAATGTCCTCTTGTGCTGCTGCGAGAGTGGCTGGCC 797
Db 804 CGCGCTCAGAGCGCGCGGCGCGGAGCGTCAACGTGGTGTGTCGAGAGCGGGTGGCC 863
Qy 798 GTACGCGCGCGGACAGCGCGGAGCGGTGTCTTAATGCGCAGACTTACAAATTTCAATTTGAT 857
Db 864 GTGCGCGCGCGGACGCGGCGGAGCAACCGGACAAACGCGCAGAGCTACACCAAGCACTCAT 923
Qy 858 CAACCATGTGGTTCAGGGGACGCGGAGCGCGGAGCGCGGCGGATTTGAGACCTTACATATTTGC 917
Db 924 CAACCATGTGGGCAAGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGG 983
Qy 918 CATGTTCAACGAGATCAGAGCGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 977
Db 984 CATGTTCAACGAGGACAGAGAGCGCGGCGCGGCTGAGATCGAGAGCACTTTGGGCTCTTCAA 1043
Qy 978 CCCTAACGAACAGCCTGTCTATTTCGATCAGCTTC 1011
Db 1044 CCGGACAAATCGCGCGGTACCCCATCAGTTTC 1077

RESULT 4

US-09-892-635A-17
; Sequence 17, Application US/09892635A
; Publication No. US20030226175A1
; GENERAL INFORMATION:
; APPLICANT: May, Gregory D.
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Mason, Hugh S.
; APPLICANT: Lim, Miguel A. Gomez
; APPLICANT: Artzen, Charles J.
; TITLE OF INVENTION: DNA Regulatory Elements Associated with Fruit Development
; FILE REFERENCE: 031998-007
; CURRENT APPLICATION NUMBER: US/09/892,635A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/160,351
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: US 60/060,062
; PRIOR FILING DATE: 1997-09-25
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 3559
; TYPE: DNA
; ORGANISM: Musa acuminata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(3559)
; OTHER INFORMATION: Complement
US-09-892-635A-17

Query Match 36.9%; Score 415.6; DB 3; Length 3559;
Best Local Similarity 68.2%; Pred. No. 6e-119;
Matches 670; Conservative 0; Mismatches 294; Indels 18; Gaps 6;

Qy 75 AGGCGTGAATCCCAATTTGGGTCTGCAATGGAATGAGCGGTGCAACACCTTCCCGGAGCGCGC 134
Db 2078 AGGAGTGCATCGATTGGTGTCTGCTACGGAATGCTCGGCAACAAATCTTCCCGCGCCAG 2137

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QY 135 CGAGCTCTCAACCTCTAAGTCCAAACAATAGCTGGCATGGACTCTACGCCGGA 194
Db 2138 CGAGTGTGCTAGTCTCTAAATCAACAATCGGAGGATGAGACTCTACGATCCAAA 2197
QY 195 CCAAGCCACTCTCCAGGCGCTCCAGGCTCTAAACTATCACTCACTCCGACGTCGCCAA 254
Db 2198 CCAAGCGGCTGCAAGCCCTCAGAACTCCAACTCCAGTCTCTGTTGGATGTCGCCG 2257
QY 255 CTCGACCTCCAAAATGCTTCGACCAATTCGCGCCGCAACTGGTTCGCAACCAA 314
Db 2258 ATCCGACGTCAGTCACTGGCTCCAACTCTTCGCGCGCGCGGACTGGATCCGAGGA 2317
QY 315 GGTCCAAAGCTTAC---CCAAAGTTGCTTCGATACATCGCGTCGGAAGAGTCA 371
Db 2318 GGTCTGCGCTACTCGCGGAGTCTCTTCGATACATAGTCTCGGAACGAGCTGAT 2377
QY 372 CCGCGG---CGGCAAGCTCAAGTCTCTCCAGCCATGAACAACATACAGTCCGCGCT 428
Db 2378 CCGCGATCGGATCTGGCGAGTACATCTCCCGCCATGGCAACATCTACATGCTTT 2437
QY 429 CTCCTCTCGCGGCTTCAGAAC---ATCAAGTCTCCATCAGTCTCTTCGCGGTCGT 485
Db 2438 GTCTCTCGGCTGGCTTCGCAAAACAGATCAAGTCTCGACCGCGTCCGACAGCGGCTCT 2497
QY 486 CGGTACTCATATCCCGCTCAGCTGGCTCTCTCTTCGATGATCGTTCGACATGGG 545
Db 2498 CGGACGCTCTACCTCTCCGCGCGGCTCTCTCTCCCGCGGCGGCTACCTGAG 2557
QY 546 TCCATCATACAGTTTCTAGCAGCAATGGCTTCCCGCTTCTTCTGCAACATCTACCCCTA 605
Db 2558 CCGCATCTGTCGATCTTGGGAGTAAAGGAGCGGCTCTCTGTCATGTTGACCTTA 2617
QY 606 CTGAGCTATGCTGCAACTCGGATCCATCGACCTCTCATACGCGCTCTTTACTGATC 665
Db 2618 TTTAGCTACACCGCAACCGGAGAGATCTCGCTGCGCTACGCGCTGTTCAAGCGCTC 2677
QY 666 TGTGACTCTGACAGGAGGCTCTAGCTTACAAACATCTTCGATGCCATGGTGA 725
Db 2678 CGCGCTCTGTCGAGGATGGCGATCAGCTATCAGAACTGTTTCGACGCGCATCGTGA 2737
QY 726 CGCATTTGCTCGGCTCGAGAGCGCGGAGCGGAGTCTCTGCTGTTGCTGCTGGA 785
Db 2738 CGCGCTCTTCGCGGCTGAGAGAGTGGAGGCGGAGAACTGGCGGTTGGTGTGCGA 2797
QY 786 GAGTGGCTGGCGCTCAGCGGCGGAGACAGC---GGCGACGGTGTCTAATGCGCAGACTTA 842
Db 2798 GAGCGGCTGGCGCTCGCGGCGGAGAGCGGAGCGGAGCAGCAACCGCGCAGACGTA 2857
QY 843 CAATTCCAATTTGATCAACCATGTTGGTTCAGGAGCGGAGAGCGGCGGAGGAT 899
Db 2858 CAACAGAACTTGATCAGGCAATGTTGGCGGAGGAAACGCGGAGAGCAGGGAAGGAT 2917
QY 900 TGAGACCTACATATTTGCGATGTTCAACGAGGATCAGAAAGCAGCGCAAGGATGAGAA 959
Db 2918 CGAGGATACATATTCGAGATGTTCAAGAGAACAGCA---AGGCTGGAGGATGAGCA 2974
QY 960 TAACTTTGGGCTGTTTTACCTTAACGAAACAGCTCTCTATTGATCAGCTCACTTGAGA 1019
Db 2975 GAACTTTGGGCTGTTTTATCCCAACAGCAGCGCGGTATACCAATAAAGCTTTAGAACT 3034
QY 1020 AATTGATCAGATGAATATAA 1041
Db 3035 AACTTTAAGGTTGATGAATCA 3056

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RESULT 5
US-10-739-930-5007
; Sequence 5007, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

```

; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10739,930
; FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 5007
; LENGTH: 1458
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER494_2
US-10-739-930-5007

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Query Match 35.0%; Score 394.2; DB 8; Length 1458;
Best Local Similarity 64.9%; Pred. No. 2e-112;
Matches 617; Conservative 0; Mismatches 328; Indels 6; Gaps 2;

QY 75 AGCGGTGGAATCCATTCGGGTCTGCAATGGAATGGAGGTGACAACTCCCGCCAGCCGCG 134
Db 108 AGCGGTGGAATCCATTCGGGTCTGCAATGGAATGGAGGTGACAACTCCCGCCAGCCGCG 167
QY 135 CGAGCTGCTCAACCTCTCAAGTCCAAACAATAGTGGCATGCGACTCTTACAGCCCGGA 194
Db 168 CACGCTGCTGAGCATGTTCAAGTCCAAACGGTATCAACTCCATGCGGCTATATGCCCCGA 227
QY 195 CCAAGCCACTCTCCAGGCGCTCCAGGCTCTTAAACATCTTACCTCATCTCGAGTCCCAA 254
Db 228 CCAGCGCGCTGTCAGGCGCTTGGCGGTACGGGCTCAACGTCTGCTGCGGGCGGCTTAA 287
QY 255 CTCCGACCTCCAAACATTTGCTCCGACCAATTCGCGCGCCCAACCACTGGGTCCAAACCAA 314
Db 288 CGAGCTGCTCTCAACCTCTGCGCGCAGCGCGCGCGCGCGCTCTGGTGGTTCAGGAGCAA 347
QY 315 GGTCAAAGCTTACCCAAAGTTCCTTCGCGATCAATCGCGCTCGGAAACGAAGTCAATCCC 374
Db 348 CATCAGCGCTTACCCGAGGTTCTCTTCGCTGCTGCTGCGTCCGCAACGAGG---TCGC 404
QY 375 CGCGGCGCAAGCTCAGTACGCTCCCGACCATCAACCAATAGTCCGCGCTCTCCCTCTCCTC 434
Db 405 CGCGGCTGCCACCGAGAACCTCTGCTCCGCGCATGAAACCACTGCGAGGCGCGCTCGCTC 464
QY 435 TGCGGCGCTTCAGAACATCAAGTCTCCATCAGTCTCTTCGCGCTGCTGCGTCACTC 494
Db 465 CGCTGGCTGGCGCACATCAGGTCACCACTGCTGCTGCGAGGCCATCTCCGGGCTGA 524
QY 495 ATATCCCGCTCAGTGGCTCTCTCTTCGATGCAATCGCTGCGATTTGGTCCATCAT 554
Db 525 CAGCGCGCTTCCGCGGCTCTTACCGGCGAGCGGACGCGTTCATGGGCGCGCTGGT 584
QY 555 ACAGTTTCTAGCCAGCAATGGCTCCCAATTTACTTTGGCAACATCTACCCCTACTTGAGCTA 614
Db 585 GCAGTTCCTGCGCGCACCGCGCGCGCTCATGGCCAACTATACCCGTACCTGGCGCTG 644
QY 615 TGCTGGCAACTCCCGATCCATCGACCTCTCATAGCGCTCTTTTACTGTCATCTGTGACAGT 674
Db 645 GGCCTACAAACCGAGCGCATGGAATGAGCTACGGCTCTTACCGGCTTCGCGCAGCGT 704
QY 675 CGTACAGGAGCGGCTCTTACGCTTAAACAACCTCTTCGATGCCATGCTGCGAGCTTGA 734
Db 705 GGTCCAGGAGCGGCTCTTACGCTTACGAGTACCAAACTCTTTCGACACCAACCGTGGACGCTTCTA 764
QY 735 CTGCGGCTTCGAGAGCGCGGAGCGGAGTCCCTGTTGCTGCTGCGAGAGTGGCTG 794
Db 765 CACGCGCATGCGCAAGCAACGCGCGCTCCAGCTGAAGCTCTGCTGCTGCGAGAGGGGTG 824
QY 795 GCGCTCAGCGCGCGGAGCAGCGCGAGCGGTCTCTAATGCGCAGACTTACAATTTCCAAATTT 854
Db 825 GCGCTCAGCGCGCGGAGCAGCGCGGCGATCTCCGCGCAACGCGCGGATCTACACCACTACCT 884
QY 855 GATCAACCATGTTGGTTCAGGGGAGCGCGGAGAGCGCGGCGGATTTGAGACCTACATATT 914
Db 885 CATCAACCATGTTGGGCGGCGGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 944

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QY 915 TGGCAAGTTCAACGAGGATCAGAGCGCGGAGGGATGAGATAAATTTGGGCTGT 974
Db 945 CTCCATGTTCAACGAGAACAGAGGA---CAGCGCGGTGAGCAGAACTGGGCACTCT 1001
QY 975 TTACCCTTAACGAGACGCTGTCTATTTCGATCAGCTTCACTTCAGAAATTTG 1025
Db 1002 CTACCCCAACATGACAGCGTCTACCCCATCAGCTTCTGATGAGCTAGCTG 1052

RESULT 6

US-10-767-701-14878
; Sequence 14878, Application US/10767701
; Publication No. US20040172694A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 14878
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS3480_1
US-10-767-701-14878

Query Match 34.9%; Score 392.6; DB 7; Length 1633;
Best Local Similarity 63.2%; Pred. No. 6.7e-112;
Matches 643; Conservative 0; Mismatches 359; Indels 15; Gaps 2;

QY 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCATGGCATGCCATCCTCTCTGTAGTACTCTCG 63
Db 107 ATGGCGGCGCAGTGTATCGCTTCCATGCTTGCACCTGGCATTTGCTCTCTCGGACATTTGCA 166
QY 64 GCAATCTCCGAGAGGGTGGATTCATTTGGGTCTGCAATGGAATGAGCGGTGACACCTC 123
Db 167 GCATCTCTACGAGAGTCAAGCCATCGGGGTGTCTACGGGTGAACGGGACAACTG 226
QY 124 CCCAGCCGCGCAGCTGTCAACCTCTACAGTCCAAACAAATAGCTGGCATGCACTC 183
Db 227 CGTGGCGAGCGAGTGTGAACTGTACAGTCCAAAGGATCACTGATGGCATC 286
QY 184 TACAGCCCGGACCAAGCACTCTCAGGCCCTCAGGGCTTAAATCTACTCATCTC 243
Db 287 TACTTCGGGGACCAACAGCGCTCAACGCGCTGAGCGGCGAGCAACATCGGGGTGATCATG 346
QY 244 GAGCTCCCAACTCCGAGCTCCAAACATTTGCTCCGACCAATCCGCGCCACCACTGG 303
Db 347 GACGTGCCCAACACGAGACTCTTCCTCGCTGGCTCCGACCCGAGCGCGGCGGCGAGCTGG 406
QY 304 GTCCAAACCAAGCTCAAGCCTTACCAACAGTTGCTTCCGATACATCGCGCTCGGAAAC 363
Db 407 GTGAAGCAAGCTGTCAGCGGTTCCCGGGGTCAACTTCAAGTACATCGCGTCCGCAAC 466
QY 364 GAAGTATCCCGGGCGGCAAGCTCAGTACGTCTCCAGGCAATGAAACAAATACAGTCC 423
Db 467 GAGG---TCTCGGGGGGACACCAACCAATCTCTCCCGCCATCGAGAAAGTCAACTCG 523
QY 424 GCGCTCTCTCTCGCGGCTTCAGAACATCAGGTCTCCATCATCAGTCTCTCTCGGCTC 483
Db 524 GCGCTGTCCACGCGGGGTGGGAAGATCAAGGTGTCCAGCGGGGTGACAGAGCGGCTC 583
QY 484 CTCGTACTCATATATCCCGCTCAGCTGGCTCTCTCTCTCGATGTCATCGTGCACATTG 543
Db 584 ACGCAGGGGTACCCCGCTGCGAGGGGAGCTTCTCTCGAGAGGTAC-----ATG 631
QY 544 GGTCCAAATACATAGTTTCTAGCCAGCAATGGCTCCCATTAATCTTGGCAACATCTACCCC 603

Db 632 GCGCCCATCGCGCAGTACTCTGACAGACACGCGGGGCGCCGCTCTCTCTCAACCGCTCTACCCC 691
QY 604 TACTTGGAGCTATGCTGGGCAACTCCGATCCATCGACCTCTCATAGCCCTCTTTTACTGCA 663
Db 692 TACTTCTCTACACGGGCAACGAGGCCAGATCGCCCTCAGCTACGCGCTCTTCAAGCTG 751
QY 664 TCTGTGACAGTGTGTAAGGACGCGGTCTTACGCTTACAAACAACTCTTTCGATGCCATGGTC 723
Db 752 CGGGGACCGTCTGTCAGGACGCGGACCAACGGGTACCAAGACCTCTTTCGACGGGCTGCTC 811
QY 724 GACGATTTGTACTCGGCCCTGAGAGCGCGGAGGCGGCGGAATGTCCCTGTCTTCGCTGTCG 783
Db 812 GACACTTTCGTTCGCGCTCGAGAAACGCGGCGCGCGGAAAGCTCGGGCTCTGCTGCTGCC 871
QY 784 GAGAGTGTCTGCGCTCAGCGCGGGGACACGCGGAGCGGTCTCTTAATGCGCAGACTTAC 843
Db 872 GAGAGCGCTGCGCTGCGCGCGCGGACGCGCCGACGCGGGGAAACGCGCAGACCTTAC 931
QY 844 AATTCCAATTTGATCAACCATGTGGTTCAGGGGACGCGGAGGCGGCGGCGGCGGCGGCGG 903
Db 932 AACCAAGACCTCATCAACCATGTGGGAAAGGCGACGCCCAAGCGGCCCGGCGCCATCGAG 991
QY 904 ACCTACATATTTGCCATGTTCAACGAGGATCAGAGAGCGCGGCAAGGGAATGAGAAATAC 963
Db 992 ACCTACATCTTCGCCATGTTCAACGAGGACAAAGAGCGGAGCGGAGCGGAGGCGAC 1051
QY 964 TTTGGGCTGTTTATACCTTAACGACAGCGCTCTTATTCGATCAGCTTCACTTGAGAA 1020
Db 1052 TTGGAGCTCTTCAACCCCGGACAAATCGCGCGGCTACTCCATCAATTTCTCTCTAAAAA 1108

RESULT 7

US-10-425-115-67183
; Sequence 67183, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 67183
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_161268C.1
US-10-425-115-67183

Query Match 34.2%; Score 384.8; DB 8; Length 1410;
Best Local Similarity 63.1%; Pred. No. 1.7e-109;
Matches 631; Conservative 0; Mismatches 357; Indels 12; Gaps 2;

QY 18 CATCATCTCCATGGCTGCCATGGCATCCCTCTTGTAGTACTCTCGCAATCCCGAGAGG 77
Db 187 CGTCGCTTCCATGTCATCGCTGGCATTTGCTTCTCGAGCATTCGACGCAATTCCTACAGG 246
QY 78 CGTGGATCCATTTGGGTCTGCATGGAATGAGCGGTGACAACTCCCGGAGCGCGCA 137
Db 247 AGTCCAAATCCATCGCGCTGTGCTACGCGGTGAACGCGGACAACTTGCCTCCGCGGAGCGA 306
QY 138 CGTGTCAACTCTTACAAAGTCCAAACATAGTGGCATGCGACTCTTACAGCCCGGACCA 197
Db 307 CGTGTGAGGTGTACAGGTCCAAAGGATCAACCTGATGCGCATCTACTTCCGAGCGC 366
QY 198 AGCCACTCTCAGGCGCTCTTAAACATCTACTCTCATCTCTCGACGCTCCCAACTC 257
Db 367 GAAAGCGCTGAACGCGCTGAGCGGACACGATCGGGCTCATCTGAGAGCTGCGCCACAC 426

QY 978 CCTAACGAAACGCTGTCTATTGATCAGCTTCACTTGA 1017
|||
Db 1035 CCGGACAAATCGCGCGGTACCCCAATTAATTTCTCTAA 1074
|||

RESULT 9

US-10-437-963-16329
; Sequence 16329, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 16329
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22088C.1
US-10-437-963-16329

Query Match 32.6%; Score 366.4; DB 7; Length 1014;
Best Local Similarity 61.5%; Pred. No. 8.8e-104;
Matches 624; Conservative 0; Mismatches 381; Indels 9; Gaps 2;
QY 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCGATGGCATCCCTCTTGTAGTACTCTCG 63
Db 1 ATGGCAAGCATGGTGTCTCCATTTTAACTGGCACTGGCTCTTGGAGTACTTGG 60
QY 64 GCATCCCGAGAGGGGTGATCCATCTGGGTCTCAATGATGAGAGGTGACAACTC 123
Db 61 CTCCTCTCAAGTCTGATGCGCGCCGCAAGCGCTCTGATGCGCAGCTGATCTGCT 120
QY 124 CCCAGCGCGGAGCTGCTCAACCTCTACAGTCCAAACATAGTGGCATCGGACTC 183
Db 121 GCGGCGCGCGGATGTCTGCGGCACTGCTGATGCGCGCGGATGCGGATGCGGATG 180
QY 184 TACAGCCCGGACCAAGCACTCTCCAGGCGCTTCCAGGCTCTTAAATCATCTATCTC 243
Db 181 CCGGCAATGCTCGCGCGCCATCGATGCCATAACCGGCTCAACATCGCCCTCACCATG 240
QY 244 GACGTCCCAACTCGACTCGACTCAAAACATTGGCTCCGACCAATCGCGCGCCCACTGG 303
Db 241 GCGGTGCGCAAGAGAACTCTCCGCGTTCGCTCCGACCGCTCCGCGTGGCCAAATGG 300
QY 304 GTCCAAACCAAGCTCCAGGCTTACCCAAAGCTTTCGATCATCGCGTGGGAAC 363
Db 301 GTCAGGAGAAAGCTCAGGTCTACCCCGGGCGTCAACTTCCGCTATCATCGCGTGGCAAC 360
QY 364 GAAGTATCCCGGCGGCAAGCTCAGTACGCTCTCCAGGCGCATGAACAAATACAGTCC 423
Db 361 GAGG---TTGAGAGGGCAACAGCGAGAAAGTCTCCGCGCATGCGAATGACAGC 417
QY 424 GCGTCTCTCTGCGCGGCTTCCAGAAATCAAGGTCTCCATCATGCTCTCTTGGGGTC 483
Db 418 GCGTCTCTGCGCGGCTTCCAGAAATCAAGGTCTCTGCTGCTGCTCCAGAGGGC 477
QY 484 GTCGTACTCATATCCCGCTCAGCTGCTCTCTCTTCCGATGCTATCGTGCACATTTG 543
Db 478 GTGTCGCGGGTACCCCGCGTCCAAATGGCATGTTCTCCCCCGAAGCACCTCGTACATG 537

QY 544 GGTCCAATCATACAGTTTCTAGCCAGCAATGGCTCCCATTTACTTTGCCAACATCTACCCC 603
Db 538 ACGCCCATCGCAAGTACTCTGGCGAGCACCGCGCGCGCTGATGGCACAAGTCTTACCCC 597
QY 604 TACTTGAGCTATGCTGGCAACTCCCGATCCAT-----CGACTCTCATACGCCCTCTTT 657
Db 598 TACTTCGCTTACGTGGGCAACCTCGCGGCGCCAGATCGACGACATCAACTACGCGCTCTTC 657
QY 658 ACTGCATCTGGTACAGTGTACAGGACGGGTCTTACGGTTTCAACAAACCTCTTTCGATGCC 717
Db 658 ACGTCGCGCGGACAGTGTGTGCGGACGGCAGCAAGGTTCACGAAACAGTTCGACGCC 717
QY 718 ATGTCGACGCAATGTACTTCGGCTCTGAGAGCGCGGAGGCCGAAATGTCCTCTGTTGTC 777
Db 718 ATCGTCGACACGTTCTACTCTCGCGCTGAGAGCGCGCGCGGAGCGTCCCGATCGTG 777
QY 778 GTGTCGAGAGTGGTGGCGCTCAGCGCGGGGACAGCGCGGACCGGTCTTAATGGCGAG 837
Db 778 GTGTCGAGAGCGGGTGGCGCTCGCGCGCGGACAGCGCGGAGCGCCAGCAACCGCAG 837
QY 838 ACTTACAATTCCAATTTGATCAACCATCTGGTTCAGGGGAGCGCCGAAGAGGCGCAGGGCG 897
Db 838 ACGTACAACCAAGACCTGTCAACACGTGCGGAGGGGAGCGCCGAGAGGGCCGAGAGA 897
QY 898 ATTGAGACTTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCGCAAGGGATTGAG 957
Db 898 ATCGAGATCTACATTTTCGCAATGTTCAACGAGTACGACAAGMAAGGCGCGACACCGAG 957
QY 958 AATAACTTTGGGCTGTTTACCCCTAACGAACAGCTGTCTATTGATCAGCTTC 1011
Db 958 AAGCACTTCGCGCTCTTCAACCCGATCAGTCGCGCGGCTTACCAATTAATTTTC 1011

RESULT 10

US-10-437-963-97429
; Sequence 97429, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97429
; LENGTH: 1898
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95433C.1
US-10-437-963-97429

Query Match 31.6%; Score 355.4; DB 7; Length 1898;
Best Local Similarity 60.8%; Pred. No. 3.5e-100;
Matches 616; Conservative 0; Mismatches 391; Indels 6; Gaps 2;
QY 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCGATGGCATCCCTCTTGTAGTACTCTCG 63
Db 214 ATGGCTAGCCAAAGGTGAGCTCCATGTTCTGCTCTCGCATGCTCTCGTGGCTTTCG 273
QY 64 GCATCCCGAGAGCGGTGGATCCATTTGGGTCTGCAATGGAATGGAAGGTGACAACTC 123
Db 274 TCCATTCCTCAAAAGCGGAGCGGATCGGGGTGTGCTACGGCATGAGCGCAACCTG 333
QY 124 CCCAGCGCGCGGAGCTGCTCAACCTCTTACAAGTCCAAACATAGTGGCATGCGACTC 183


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Db 334 CGCGCGGAGTCGTCGGTGGGATGTCACGCTCAAGGGATCAGTCGATGGGGTG 393
Qy 184 TACAGGCGGACCAAGCACTCTCAGGCGCTTCAAGGCTTTAAACATCTACTCATCTC 243
Db 394 TACGCGCGGACCAAGCGGCTGTCAGTGGTGGGCGACGGGATCAGCGTCTGTCGTC 453
Qy 244 GAGCTCCCAACTCCGACTCCAAACATTTGCTCCGACCAATCGCGCGGCGCAACTGG 303
Db 454 GCGCGCGCAAGACGTCCTTCCAACTCCGCGCGGCGCGCGCGCGCGCTGTCGTCG 513
Qy 304 GTCCAAACCAACGCTCAAGGCTTACCAAAAGTGTCTTCCGATACATCGCGCTCGGAAC 363
Db 514 GTGCGGAACACATCAGGCTTACCGCTCGGTGTGTTCCGGTACGTCGCGTGGGAAC 573
Qy 364 GAAGTCATCCCGCGGCGCAAGCTCAGTACGTCCTCCAGGCAATGAACAAACATACAGTCC 423
Db 574 GAGG---TCGCGCGGCGGCGCACGTCACGCTGGTCCCGGCAATGGAGAACTTCGGGGC 630
Qy 424 GCCCTCTCTCTGCGCGGCTTCAGAACATCAGGTCCTCAATCAGTCTCTTTCGGCGTC 483
Db 631 GCGCTGGTGTGCGGCGGCTGGGCGACATCAAGGTGACGAGCTCGGTGTCCAGCGCTC 690
Qy 484 CTCGCTACTCATATATCCCTCAGTGGCTCTCTCTTCGATGCAATCGTCGACATTTG 543
Db 691 CTCGCGGTGTACAGCGCGGCTTCGCGCGGAGTTACCGGGGAGTCGCGGCTTCATG 750
Qy 544 GGTCAATCATACAGTTTTCAGCAGCAATGGCTCCCAATTAATCTTTCGCAACATCTACCCC 603
Db 751 GCGCGCGCTCTGAGCTTCTCGCGCGCACCGCGCGGCTGCTCGCGCAACATCTACCCC 810
Qy 604 TACTTGACTATGCTGGCAATCCCGGATCCATCGACTCTCATAGCCCTCTTTACTGCA 663
Db 811 TACTTCTCTACACCTACAGCCAGGGCAGCGCTCGAAGCTCTCTACGCGCTCTTTCACCGCC 870
Qy 664 TCTGTACAGTCGTACAGAGCGGTTCACGCTTACAAACACCTCTTCGATGCGCATGTC 723
Db 871 GCGCGCACGTCGTTCAGACAGCGGCTTACGGGTACAGAACCTGTTTCGACACACCGTC 930
Qy 724 GACGATTTGATTCGCGCTTCAGAGAGCGCGGAGCGCGAATGTCCCTGTTGTGTCGTCG 783
Db 931 GACGCTTTACGCGGCTATGGCAAGCAGCAGCGGCTCCGCGCTCTCCTCTGTCCTCC 990
Qy 784 GAGATGCTGCGCTTCAGCGGCGGAGCAGCGGCGAGCGGTGTCTAATGCGCAGCTTAC 843
Db 991 GAGACCGGCTGGCCCTTCGCGCGGCGGATGTCCGCTCTCGCGCGCAACGCGCGATCTAC 1050
Qy 844 AATTCCAATTTGATCAACCATGTGGGTTCAGGGAGCGCGAAGAGCGGCGGCGATTCAG 903
Db 1051 AACCGAACCTCATACACACGTCGCGCGGCGACGCGCGCGCACCCCGCGCATCGAG 1110
Qy 904 ACCTACATATTTGCAATTTCAAGAGATCAGAGAGCGCGCAAGGGAATGAGAAATAC 963
Db 1111 ACCTACGCTTCTTCCATGTTCAACAGAAACAGAGGAGCGC---CGGCGTCGAGCAGAT 1167
Qy 964 TTTGGCTGTTTACCTTAAAGACAGCTGTCTATTGATCAGCTTCACTTG 1016
Db 1168 TGGGCGCTCTTCTACCCCAATGACGACAGCTCTACCCCATCAGCTTCTGATG 1220
```

RESULT 11

US-10-259-165-439/c

; Sequence 439, Application US/10259165

; Publication No. US20030135888A1

; GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Wang, Xun

; APPLICANT: Chang, Hur-song

; APPLICANT: Briggs, Steven P.

; APPLICANT: Cooper, Bret

; APPLICANT: Glazebrook, Jane

; APPLICANT: Goff, Stephen A.

; APPLICANT: Katagiri, Fumiyaki

```
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 439
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-439
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Query Match 31.5%; Score 354.2; DB 6; Length 1110;

Best Local Similarity 60.9%; Pred. No. 6.3e-100;

Matches 613; Conservative 0; Mismatches 388; Indels 6; Gaps 2;

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Qy 4 ATGGGAGCTCAGCACATCTCCATGGCTGCCATGGCATCCCTCTTGTAGTACTCTCG 63
Db 1029 ATGGCTAGCCAAAGGTGTAGCCTCCATGTTCTCTCGCATGCTCTCGGTGCTTGGC 970
Qy 64 GCATCCCGAGAGCGGTGGATCCATTGGGGTCTGCATGGAATGGAGCGGTGACAACTC 123
Db 969 TCCATTCTCTAAAGGCGGAGCGCATCGGGGTGTGCTACGGCATGAGCGCAACACTG 910
Qy 124 CCCAGAGCGCGGACGCTGCTCAACTCTACAAGTCCAAACATAGCTGGCATGCGACTC 183
Db 909 CCGCGGCGGAGCTCGGTGGTGGGATGTACCGCTTCCAAAGCATCATCGTCATGGGCTG 850
Qy 184 TACAGCCCGGACCAAGCACTCTCCAGGCCCTCCAGGGCTCTAACTATCTATCTCTC 243
Db 849 TACGCGCGGACCAAGCGGCGCTGCTGCTGCGTGGGCGGCGACGGGATCAGCGTCTGTC 790
Qy 244 GAGCTCCCAACTCGGACTCCAAACATTTGCTTCCGATACATCGCGCGGCGCAACACTGG 303
Db 789 GCGCGCGGCAACGACGCTCTCTCAACTCTCGCGCGCAGCCCGCGGCGGCGCTGTCG 730
Qy 304 GTCCAAACCAACGCTCAAGCCTTACCCAAACGTTGCTTCCGATACATCGCGCTCGGAAC 363
Db 729 GTGCGGAACACATCCAGGCTTACCGCTGCTGCTGCTTCCGTTAGCTCGCGTGGGAAC 670
Qy 364 GAGTCTATCCCGCGGCGCAAGCTCAGTACGTCCTTCCAGCCATGAACAAATACAGTCC 423
Db 669 GAGG---TCGCGCGGCGGCGCACGCTCCAGCTGGTTCGCGCATGGAGAACGTCCGCGC 613
Qy 424 GCGCTCTCTCTGCGGCGCTTCAGAACATCAAGGCTCTCCATCAGTCTCTTTCGGCGTC 483
Db 612 GCGCTGCTGCTGCGGCGGCTGGGCGCATCAAGGTGACAGCTCGGTGTGCGAGCGCTC 553
Qy 484 GTCGGTACTCATATCCCGCTCAGCTGGCTCTCTTCTTCCGATGATCTGTCGACATG 543
Db 552 CTCGCGGTGTACAGCGCGGCTTCGCGCGGAGTTCAACGGCGAGTCGACGGGCTTCATG 493
Qy 544 GGTCCAAATCATACAGTTTCTAGCCAGCAATGGCTCCCAATTTACTTGGCAACATCTACCCC 603
Db 492 GCGCGCGCTCTGAGCTTCTCGCGCGCACCGCGCGGCGGCTGCTCGCGCAACATCTACCCC 433
Qy 604 TACTTGAGCTATGTGGCAACTCCGGATCCATCGACTCTCATAGGCTCTTTCATCTGCA 663
Db 432 TACTTCTCTACACCTTACGCGGAGCGGTGCGAGCTCTCTTACCGCTCTTTCACCGCC 373
Qy 664 TCTGTACAGTCGTACAGGAGCGGTCTCTAGCTTTACAAACACTCTTTCGATGCCATGTC 723
Db 372 GCGGCGACCGTCTGTCGAGGACGGGCGCTTACGGGTACCGAGAACCTTGTTCGACACCGCTC 313
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QY 724 GACGATTTGATCTCGGCTTGGAGAGCGCGGAGGCCGGAATGTCCCTTTGTCTGTGTCG 783
DB |||||
DB 312 GACGCTTTCTAGCGCCCATGGCAAAGCAACGCGGCTCGGGGTCTCCCTCGTCTCTCC 253
QY 784 GAGAGTGGCTGGCGCTCAGCGGGGGAAGCGGCGACGGTGTCTTAATCGGACATTTAC 843
DB |||||
DB 252 GAGACAGGCTGGCGCTTCCGCGGCGCATGTCCGCTTCCGCGGCAACCGCGGATCTAC 193
QY 844 AATTCCAAATTTGATCAACCATTTGGGTCAAGGGAAGCGCGGAGCGGCGGCGATTGAG 903
DB |||||
DB 192 AACCAGAACTCATCAACCAACGTCGGCGCGGCAACCGCGGCGGCGGCGGCGGCGG 133
QY 904 ACTTACATATTTGCCATTTTCAACGAGGATCAAGAGCGGCGGCGGCGGCGGCGGCGG 963
DB |||||
DB 132 ACTTACATTTCTTCCATTTTCAACGAGGATCAAGAGCGGCGGCGGCGGCGGCGGCGG 76
QY 964 TTTGGGCTGTTTACCTTAAACGAGCGCTGTCTATTTCATCAGCTT 1010
DB |||||
DB 75 TGGGGCTCTTTTACCCCAACATGACGACGCTTACCCCATCAGCTT 29

RESULT 12

US-10-259-165-105/c
; Sequence 105, Application US/10259165
; Publication No. US2003013588A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiya
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: US/030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 105
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-105

Query Match 31.4%; Score 353.8; DB 6; Length 1113;
Best Local Similarity 60.7%; Pred. No. 8.4e-100;
Matches 615; Conservative 0; Mismatches 392; Indels 6; Gaps 2;
QY 4 ATGGCAGCTCAGCACATCATCTCCATGCTGCGATGGCATCCCTCTTGTAGTACTCTCG 63
DB |||||
DB 1029 ATGGTACCGAAGGTGTAGCTCCATGTTGCTCTGCAATGCTCTCTCGTGGCTTTGCC 970
QY 64 GAAATCCGAGAGCGGTGGAATCCATTTGGGTTCTCAATGGAATGAGACGGTGACAACCTC 123
DB |||||
DB 969 TCCATTCTCAAAGCGGAGCGGATCGGGGTGTCTACGGCATGAGCGGCAACACCTG 910
QY 124 CCCAGCGCGGCGAGCTGTCACCTTACAGTCCAAACATAGCTGGGATCGGATC 183
DB |||||
DB 909 CCGCGCGGAGCTCGGTGGTGGGATGTACCGCTCCACGGCATCACGTGATGGGCTG 850

QY 184 TACAGCCCGACCAAGCCCACTCTCTCAGGCGCTTCCAGGCGCTTAAACATCTACCTCTCTC 243
DB |||||
DB 849 TACGCGCGGACAGCGGCGCTGCTGAGTGGTGGGCGGCGGCGGATCAGCGCTCGTCTGTC 790
QY 244 GAGCTCCCGCACTCCGACCTCAAACATTTGCTTCCGACCAATTCGCGCGGCAACCACTCG 303
DB |||||
DB 789 GCGCGCGCCCAACGACGTGCTCTTCCAACTTCCGCGGCGGCGGCGGCGGCGGCTGCTG 730
QY 304 GTCCAAACCAAGCTTACCAAGCTTACCAAGCTTACCAAGCTTACCAAGCTTACCAAGCT 363
DB |||||
DB 729 GTGCGGAAACATCAAGGCTTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 670
QY 364 GAAGTATCTCCCGCGGCGCAAGCTCAGTACGCTCTCTCCAGCCATGAACCAACATACAGTCC 423
DB |||||
DB 669 GAGG---TCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 613
QY 424 GCGCTCTCTCTGCGCGGCGGCTTCAAGAAATCAAGGCTTCAAGGCTTCAAGGCTTCAAG 483
DB |||||
DB 612 GCGCTGGTGTGCGGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTC 553
QY 484 GTGCGTACTCATATATCCCGCTCAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 543
DB |||||
DB 552 CTCGCGGTGTACAGCGCGGCGGCTTCCCGCGGAGTTTACCGGCGGAGTTCGCGGCGGTT 493
QY 544 GGTCCAAATCATAAGTTTCTAGCCAGCAATGGCTCTCCCAATTAATTTGCGCAACATCTACCC 603
DB |||||
DB 492 GCGCGCGCTCTGAGCTTCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 433
QY 604 TACTTGAGCTATGCTGGCAATCTCCGAGTCTCTGAGCTCTCTATACGCGCTCTTTTACTGCA 663
DB |||||
DB 432 TACTTCTCTTACACCTACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 373
QY 664 TCTGTGAGCTGCTACAGGCGGCTTACGCTTCAACCAACCTCTTCTGATGCGGCTGCTC 723
DB |||||
DB 372 GCGGCGCGCTGCTCAGGAGCGGCGGCTTACGCGGTTACGAGAACTTCTTCTGACACCGG 313
QY 724 GACGATTTGATCTCGGCGCTTGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 783
DB |||||
DB 312 GACGCTTCTAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 253
QY 784 GAGAGTGGCTGGCGCTTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 843
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DB 252 GAGACAGGCTGGCGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 193
QY 844 AATTCCAATTTGATCAACCATTTGGGTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 903
DB |||||
DB 192 AACCAGAACTCATCAACCATCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 133
QY 904 ACCTACATATTTGGCATTTTCAAGAGGATCAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 963
DB |||||
DB 132 ACCTAGCTTCTTCCATTTTCAACGAGAAACGAGGAGGAGCG---CGGCGTCCGAGCAAT 76
QY 964 TTTGGGCTGTTTACCTTAAACGAGCGCTGTCTATTTCGATCAGCTTCTCAGCTT 1016
DB |||||
DB 75 TGGGCGCTCTTCTTACCCCAACATGACGACGCTTACCCCATCAGCTTCTGATG 23

RESULT 13

US-10-425-114-20801
; Sequence 20801, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28


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QY 721 GTCGACGCAATTGTACTCGGCCCTCGAGAGCGCCGAGGGCCGGAATGTCCCTGTTGTCTCGTG 780
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 760 GTGACGCGCGTGTACGCGCGGTGAGAGAGGCCCGCGCGCGCGGTGAAGTGTGTGTG 819
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 781 TCGGAGAGTGGCTGGCCCGTCAAGCGGGCGGGACAGCGCGACGGTGTCTTAATCGCGAGACT 840
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 820 TCGGAGAGCGGGTGGCCGTTCGGCGGGCGGGTTTGGCGGTTCGGCCGGCAATGCGCGGACG 879
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 841 TACAATTCGAATTTGATCAACCATGTGGGTCAAGGGACGCCGAGAGAGGCCAGGGGCGATT 900
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 880 TACAACCAAGGGCTGATCAACCCACGTTCGGCGGGGGCACGCCCAAGAGAGGGAGCGCTG 939
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 901 GAGACCTACATATTGCGCATGTTCAACGAGGATCAGAGACAGCCCAAGGGATTGAGAT 960
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 940 GAGCGTACATCTTCGCCATGTTCAACGAGAACCCAGAGACCGGGGACGCCACGGAGAGG 999
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 961 AACTTTGGGCTGTTTACCTAAACGACAGCCTGTCTATTGATCAGCTTC 1011
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1000 AGCTTCGGGCTCTTCAACCCGGACAAGTCGCGGCGATACACATCCAGTTC 1050
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: April 7, 2006, 22:35:54
Job time : 1109 secs

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 20:54:59 ; Search time 661 Seconds
(without alignments)
6808.813 Million cell updates/sec

Title: US-10-647-649-2

Perfect score: 1125

Sequence: 1 ttcatggcagctcagcacat.....ctaattaaactataaata 1125

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_New.*

- 1: /SIDSS/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /SIDSS/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq.*
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- 13: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 14: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 15: /SIDSS/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86.2	7.7	438	11	US-11-116-881A-1842
2	86.2	7.7	491	11	US-11-116-881A-2189
3	86.2	7.7	546	11	US-11-116-881A-1704
4	80.8	7.2	386	11	US-11-116-881A-703
5	76.6	6.8	487	11	US-11-116-881A-1232
6	55.6	4.9	1330	11	US-11-096-568A-9277
7	54.8	4.9	9903	14	US-11-052-554A-517
8	49.6	4.4	1501	14	US-11-138-987-16
9	48.2	4.3	6645	14	US-11-128-061-426
10	48.2	4.3	6645	14	US-11-128-049-426
11	47.2	4.2	3486	9	US-10-932-182A-191019
12	47.2	4.2	3486	9	US-10-932-182A-191019
13	47.2	4.2	88421	14	US-11-205-109-1
14	47	4.2	142303	14	US-11-121-086-42
15	47	4.2	165911	11	US-11-114-798-52
16	46.8	4.2	2304	14	US-11-052-554A-538
17	46.8	4.2	6210	14	US-11-056-470-1
18	46	4.1	6615	14	US-11-052-554A-518

19	45.8	4.1	1108	11	US-11-096-568A-11282	Sequence 11282, A
20	45.8	4.1	4983	14	US-11-052-554A-521	Sequence 521, Appl
21	45.6	4.1	1614	14	US-11-218-780-5	Sequence 5, Appli
22	45.4	4.0	1583	11	US-11-096-568A-12501	Sequence 12501, A
23	44.8	4.0	1285	11	US-11-096-568A-4600	Sequence 4600, Ap
24	44.6	4.0	386	11	US-11-116-881A-1385	Sequence 1385, Ap
25	44	3.9	1296	8	US-10-525-674-25	Sequence 25, Appli
26	44	3.9	1517	11	US-11-096-568A-21483	Sequence 21483, A
27	43.8	3.9	773	14	US-11-110-082-3	Sequence 3, Appli
28	43.8	3.9	1167	11	US-11-228-659-19	Sequence 19, Appl
29	43.8	3.9	1731	14	US-11-052-554A-548	Sequence 548, App
30	43.8	3.9	3419	11	US-11-228-659-17	Sequence 17, Appl
31	43.2	3.8	2010	14	US-11-058-727-5	Sequence 5, Appli
32	43.2	3.8	2010	14	US-11-108-389-5	Sequence 5, Appli
33	43.2	3.8	2010	14	US-11-224-624-5	Sequence 5, Appli
34	43.2	3.8	2135	11	US-11-096-568A-11555	Sequence 11555, A
35	43	3.8	1613	14	US-11-024-959-71	Sequence 71, Appl
36	43	3.8	2562	14	US-11-052-554A-533	Sequence 533, App
37	42.6	3.8	1379	11	US-11-096-568A-16670	Sequence 16670, A
38	42.6	3.8	1741	11	US-11-096-568A-13489	Sequence 13489, A
39	42.6	3.8	57073	8	US-10-995-561-13275	Sequence 13275, A
40	42.2	3.8	4581	9	US-10-932-182A-79437	Sequence 79437, A
41	42.2	3.8	15720	14	US-11-108-172-1058	Sequence 1058, Ap
42	42.2	3.8	2250	14	US-11-052-554A-532	Sequence 532, App
43	42	3.7	1191	11	US-11-096-568A-25694	Sequence 25694, A
44	41.8	3.7	1450	11	US-11-096-568A-12512	Sequence 12512, A
45	41.8	3.7				

ALIGNMENTS

RESULT 1

US-11-116-881A-1842
; Sequence 1842, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1842
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-11-116-881A-1842

Query Match 7.7%; Score 86.2; DB 11; Length 438;

Db 228 AGATACAAATGCTTCAACGCTCTCAGAGGAAGTAACATTGAGATCATTTCTCGAGTCCC 287
Qy 252 CAATCCGACCTCGAAACATTTGCTCCGACCAATCCGCGGCCCAACTGGTCCAAAC 311
Db 288 ACTTCAAGATCTTCAATCCCTAACTGATCTTCAAGAGCCAAATGGATGGTCCAGATAA 347
Qy 312 CAACGCTCAAGCTTACCCAAAGTTGCTTCCGATACATCGCGTCGGAACGAAGTCAT 371
Db 348 CATAATAATCATTTCCAGATGTTAAATTAATATATAGTGTGGAAATGAAGTCTC 407
Qy 372 CCCCGCGGCCCAAGCTCAGTAGC 394
Db 408 TCCCGGAAATGATGCTCAATATG 430

RESULT 6
US-11-096-568A-9277
; Sequence 9277, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 9277
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1330)
; OTHER INFORMATION: Ceres Seq. ID no. 15179743
US-11-096-568A-9277

Query Match 4.9%; Score 55.6; DB 11; Length 1330;
Best Local Similarity 45.6%; Pred. No. 2e-05;
Matches 196; Conservative 0; Mismatches 234; Indels 0; Gaps 0;
Qy 86 CATTGGGGTGTGCAATGGAATGGAGGTGACAACTCCCGCAGCGCGCGAGTGGTCA 145
Db 47 CATGGGATCTTCCCCCGCTCTCTCCGCTCTCTCCGCGCGCGCGCTCCG 106
Qy 146 ACCTCTAAGTCCAAACATAGCTGGCATGCGACTCTACAGCCCCGACCAAGCCATC 205
Db 107 CTTCCGCGCGCCAAACGACCTGGTTCGGGAGTCCAGTCCCTCGCTCCCGCTCCCG 166
Qy 206 TCCAGGCCCTCAGGGCTCTAATCTTACCTATCTCTCGAGTCCGCCAACTCCGACCTCC 265
Db 167 CCGCGTGTATCCACTCAACGACACTCCGTCAACCGCTTCTCTCTCGCGCGCGCGC 226
Qy 266 AAACATTTGCTCCGACCAATCCGCGCCCACTGGGTCCAAACCAACTCCAGGCT 325
Db 227 GCGCCCTACTCGTCTCTGCTTTCTCGACGCGCACCCTCGCTCACTCCAAAGACCGACTCC 286
Qy 326 ACCCAAGCTTGGCTTCCGATACATCGCGCTCGGAACGAAGTCAATCCCGCGCGCCAAAG 385
Db 287 ACCTCCCGAGCTCGCGCGAGTTGGGCTCTCTCGCTCTCTTCCAGCCCAACACC 346
Qy 386 CTAGTAGTCTCCCGACGATGAACAATACATAGTTCGCGCTCTCTCTCTCGCGCGCTTC 445
Db 347 CCGACTCTCGGACCTCTTCTTCCGCGACATCGAGTTCTCGAGTTCGAGCACTCTTCT 406
Qy 446 AGACATCAAGTCTCCACATCAGTCTCTTCGGGCTGTGGTACCTCATATCCCGCT 505
Db 407 CCGAGTCGGGTCAACTCTCTCCCGACGTCGCGCTCATCCGCGCGGAGCACTCCCGCC 466
Qy 506 CAGCTGGCTC 515
Db 467 TCGCGGACTC 476

RESULT 7
US-11-052-554A-517
; Sequence 517, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 517
; LENGTH: 9903
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-517

Query Match 4.9%; Score 54.8; DB 14; Length 9903;
Best Local Similarity 50.3%; Pred. No. 7.6e-05;
Matches 162; Conservative 0; Mismatches 157; Indels 3; Gaps 1;
Qy 186 CAGCGCGGACCAAGCCTCTCCAGGGCCTCCAGGGCTCTAACATCTACCTCATCTCGA 245
Db 8169 CATGCCAACCCGGGCAACCAACACCGGCTCTTCAACATCGGCACCTTCAACACCGG 8228
Qy 246 GGTCCCAACTCCGACCTTCAAAACATTTGCTCCGACCAATTCGCGGCCCACTGGGT 305
Db 8229 CATGCCAAACCGGGCCACTACAACACCGGCTCTTACAACACCGGTAGTACAACACCGG 8288
Qy 306 CCAAACCAAGCTCCAAAGCTTACCCAAAGTTGCTTCCGATACATCGCCGTCGGAAGCA 365
Db 8289 CATGCCAAACCGGGAGACTACGGCACCGGCGCTTCAATACCGGAGCATGAACACCGG 8349
Qy 366 AGTCATCCCGCGCGCAGCTCAGTACGCTCTCCAGCCATGAACACATACAGTCCGC 425
Db 8349 CTTCCTCTGGCGCGCGGAGCGGCTCTGCGGCGCACTACCATCACCATCGA 8408
Qy 426 CCTCTCTCTGCGCGCT---TCAGAACATCAAGGTCTCCACATCAGTCTCTTGGGCT 482
Db 8409 GCGACCTGCGCGCTTCTCAATGTGACATCCCGTCAACATCCCATCACCGGCGACAT 8468
Qy 483 GGTGGTACCTCATATCCCCC 504
Db 8469 CACCAATGTCTCCATCCCCGC 8490

RESULT 8
US-11-138-987-16/c
; Sequence 16, Application US/11138987
; Publication No. US20050278800A1
; GENERAL INFORMATION:
; APPLICANT: Elton, Claire K
; APPLICANT: Demmer, Jeroen
; TITLE OF INVENTION: Compositions and methods for the modification of
; FILE REFERENCE: 11001.1086U
; CURRENT APPLICATION NUMBER: US/11/138,987
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 60/580,007
; PRIOR FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1501

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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-138-987-16

Query Match      4.4%; Score 49.6; DB 14; Length 1501;
Best Local Similarity 47.5%; Pred. No. 0.0011;
Matches 213; Conservative 0; Mismatches 229; Indels 6; Gaps 2;

QY 493 TCATATCCCCCTCAGCTGGCTCTTCTTCCCGATGCAATCGTGACATTTGGGTCCAATC 552
Db 580 TCTGGTCGACCTTCTTCAGGACACTTTAGGGCTGACCTCAACAAGACGATGATTGAATC 521
QY 553 ATACAGTTTCTAGCCAGCAATGGTCCCACTTACTTGGCAACATCTACCCCTACTTGAGC 612
Db 520 CTCTCCTTTCTCACAAGCACACTCTCCTTTTGTGACAATCTCTCCTTTCTCTAAGC 461
QY 613 TATGCTGGCACTCCGGATCCATCGACTCTCATAGCCCTCTTACTGCACTCTGTACA 672
Db 460 T---TTCACGAAACAGNACATCTCCCTTGACTTTAGGCTCTTTAAAGAAACAGCAAAG 404
QY 673 GTCGTACAGGCGGTCTTACGCTTACAAACACTCTTTCGATGCCATGGTCGACGATTG 732
Db 403 GCTCACAAGACGGACGTAACACCTACAGAAACAGCTTTGATCTAAGCTATGACACACTT 344
QY 733 TACTCGGCCCTGAGAGCGCCGAGGCGGAATGTCCTCTGTTGTCGTGCGAGAGTGGC 792
Db 343 GTCTCTGCAATTGTTTCACAATTGGGTTTTCGGAGGTGGATATGTTGTGTCAAAGATCGT 284
QY 793 TGGCGCTCAGCGGGGGGACGCGCGGCTTAATGGCAGACTTACAAATTCCAAT 852
Db 283 TGGCTACAGATGAGAGGAGAAATGCAACATCACTGATCTGTGAGGCGTCTTTAAAGGA 224
QY 853 TTGATCAACCATGTGGGTGAGGGGAGCGCGGAGAGGCGGAGGCGCA---TTGAGACCTTAC 909
Db 223 CTGATAGTCTACTTGGAGAAAGAGCGCTCTCTCCGCGCTCTCTCTGTTGAACCTTAC 164
QY 910 ATATTGGCATGTTCAACGAGGATCAGA 937
Db 163 ATTGAAGTCTCTTGGACGAGATCAGA 136

RESULT 9
US-11-128-061-426
; Sequence 426, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426
; LENGTH: 6645
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4002)..(4019)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-426

Query Match      4.3%; Score 48.2; DB 14; Length 6645;
Best Local Similarity 41.7%; Pred. No. 0.0051;
Matches 204; Conservative 24; Mismatches 252; Indels 9; Gaps 1;

QY 113 GTGACAACTCCCGCCAGCCCGCGAGCTGGTCAACCTCTACAGTCCCAACACATAGCTG 172
Db 5121 GAGCCACAGCTCCCGCGGGGCTATACCCAGAGCCCTTCATCTCTCTTACTTCCACCY 5180
QY 173 GCATCGCACTCTACAGCCCGCAAGGCACCTCTCCAGGCCCTCCAGGGCTCTTAACATCT 232
Db 5181 TCCTACTCCCAACCTCGCCATCTTATTCCCAACAGTCCCAACTATAGCCCTACTRCA 5240
QY 233 ACCTCATCTCGAGTCCCAACTCCGACCTCCAAAAATTGGCTCCCGAACCAATCGCGG 292
Db 5241 CCTAGCTACTCKCCRACTCTCCATCTCTCSCCAAGCTCTCCWWSCTTACTTCMCRACC 5300
QY 293 CCACCACTGGTCCAAACCAAGTCCAAAGCTTACCCCAAGCTTCCGCTTCCGATACATG 352
Db 5301 TCTCCATCTTACTCCCRACCTCTCCAGCTTCTCCAGCTTCTCCCRACMTCTCCYAGCTACTCMCCR 5360
QY 353 CCGTCGAAAGCAAGTCAATCCCGCGGCGCAAGCTCAGTAGCTCTCCCGACCATGAACA 412
Db 5361 ACATCACCAGTACTTCCCRACCTTCTCCAGC-----TACTCCCRACATCWCCY 5411
QY 413 ACATACAGTCCGCCCTCTCTCTGCGGCCCTTCAGAACATCAAGGTCTCCACATCAGTCT 472
Db 5412 AGCTACTCACCAAGTCTCCAGCTTCTCCAGCTTCTCCCAAGTATCTCTTCTCCACCTCC 5471
QY 473 CTTGCGGCTGTCGGTACTCTCATATCCCCCTCAGCTGGCTCTTCTTCCGATGAT 532
Db 5472 CCCAGTTACTCAGCAGCTCTCCAGCTTCTCCAGCTTCTCTTCTTCTCCAGCTTCTCCGCACT 5531
QY 533 CGTGCACTTGGTCCCAATCATATAGTTTCTAGCCAGCAATGGCTCCCACTTACTTGGCA 592
Db 5532 TCTCCAGTTATTTCWCCACCAAGCCCTTAATTTCTCCAACTAGTCCCAATTAYACSCCA 5591
QY 593 ACATCTACC 601
Db 5592 ACATCMCCC 5600

RESULT 10
US-11-128-049-426
; Sequence 426, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426
; LENGTH: 6645
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4002)..(4019)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-426
```


QY 476 TCGCGCTCGTACCTCATATCCCTCCCTCAGCTGGCTCTCTCTCCGA 527
Db 826 TCTACAACCTTCTACCACTCTACCACTTCTACCACTTCTACCGCTCCCAAGA 877

RESULT 13

US-11-205-109-1

; Sequence 1, Application US/11205109
; Publication NO. US20050287641A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
; FILE REFERENCE: 3002-2US
; CURRENT APPLICATION NUMBER: US/11/205,109
; CURRENT FILING DATE: 2005-08-17
; PRIOR APPLICATION NUMBER: US/09/976,059
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,924
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
; NAME/KEY: misc feature
; LOCATION: (2077)..(3078)
; OTHER INFORMATION: ORF 1; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3118)..(4032)
; OTHER INFORMATION: ORF 2; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4038)..(5048)
; OTHER INFORMATION: ORF 3; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6665)..(5814)
; OTHER INFORMATION: ORF 4; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7703)..(6693)
; OTHER INFORMATION: ORF 5; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9464)..(8130)
; OTHER INFORMATION: ORF 6; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9691)..(10761)
; OTHER INFORMATION: ORF 7; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12751)..(10829)
; OTHER INFORMATION: ORF 8; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13617)..(12802)
; OTHER INFORMATION: ORF 9; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15203)..(13614)
; OTHER INFORMATION: ORF 10; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15591)..(15863)
; OTHER INFORMATION: ORF 11; positive strandedness
; FEATURE:
; NAME/KEY: misc feature

; LOCATION: (15880)..(19035)
; OTHER INFORMATION: ORF 12; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19032)..(39713)
; OTHER INFORMATION: ORF 13; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (39713)..(65800)
; OTHER INFORMATION: ORF 14; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65826)..(66530)
; OTHER INFORMATION: ORF 15; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (66546)..(67370)
; OTHER INFORMATION: ORF 16; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67384)..(70059)
; OTHER INFORMATION: ORF 17; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70059)..(70662)
; OTHER INFORMATION: ORF 18; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70859)..(71906)
; OTHER INFORMATION: ORF 19; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (73439)..(71964)
; OTHER INFORMATION: ORF 20; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (74216)..(73563)
; OTHER INFORMATION: ORF 21; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (75424)..(74213)
; OTHER INFORMATION: ORF 22; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (75535)..(76464)
; OTHER INFORMATION: ORF 23; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (78110)..(76449)
; OTHER INFORMATION: ORF 24; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (79864)..(78107)
; OTHER INFORMATION: ORF 25; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81624)..(79861)
; OTHER INFORMATION: ORF 26; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81909)..(81682)
; OTHER INFORMATION: ORF 27; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82346)..(82062)
; OTHER INFORMATION: ORF 28; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82587)..(84446)
; OTHER INFORMATION: ORF 29; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84481)..(85548)

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; OTHER INFORMATION: ORF 30; positive strandedness
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (85556)..(86845)
; OTHER INFORMATION: ORF 31; positive strandedness
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (87372)..(86803)
; OTHER INFORMATION: ORF 32; negative strandedness
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-11-205-109-1

Query Match          4.2%; Score 47.2; DB 14; Length 88421;
Best Local Similarity 46.6%; Pred. No. 0.028;
Matches 151; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

Qy 115 GACAACTCCCGCCAGCCGCGAGTCTGCTCAACTCTCAAGTCCAAACAATAGCTGGC 174
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52991 GCCGACCAACCCCGTCCGCGAGGCCACCTACCGCGGCCACACCGTGGAGTTACCCGTG 53050

Qy 175 ATGGACTCTACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTAC 234
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53051 CCCC CGCGCGTGCACCACTCCCGAACTCGCGCCCGCAACGGCGTCACCGTCTTC 53110

Qy 235 CTCATCTCGAGTCTCCCAACTCCGACCTCCAAACAATTGGCTCCGACCAATCCGCGCC 294
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53111 ATGACCGTGCAACCGCCTCGCGTCTCTGTCCAACTCGGCGCGGACCGACATC 53170

Qy 295 ACCAACTGGTCCAAACCAAGTCCAGCGTACCCAAAGTGTGCTTCCGATACATGCC 354
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53171 CCCATCGCGTGGCGTCCGCGAGCGCACCGACCCACCCCTCGACCAACTCATCGGCTTC 53230

Qy 355 GTCGAAACGAAGTATCCCGGGGCAAGCTCAGTAGCTCTCCAGCCATGAACAC 414
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53231 TTGCTCAACACCTTCGTCTGACACCGACCTGACCGGCAACCCACCATCACCGACCTG 53290

Qy 415 ATACAGTCCGCGCTCTCTCTGCC 438
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53291 CTGCACCGCACCCGCGACACCACC 53314
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```
RESULT 14
US-11-121-086-42
; Sequence 42, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: FOULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 142303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-42

Query Match          4.2%; Score 47; DB 14; Length 142303;
Best Local Similarity 48.0%; Pred. No. 0.039;
Matches 134; Conservative 0; Mismatches 145; Indels 0; Gaps 0;
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Qy 97 TGCATGAATGGAGCGTGACAACCTCCCGCGCGCGAGCTCGTCAACTCTTACAAAG 156
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22547 TACAACCCCATCCCGTCTCCATCATGTACAAACCCCATCCCGACCTCCATCGTGTACAAAC 22606
```

```
Qy 157 TCGAACACATAGCTGGCATCGGACTCTACAGCCCGGACCAAGCACTCTCCAGGCCCTC 216
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22607 CCCATCCCGCTTCCATCATCAGTACACCCCATCCCACTCCATCATACATCAACCCCATC 22666

Qy 217 CAGGGCTCTAACATCTACCTCATCTCGAGCTGCCCAACTCCGACCTCCAAAACATTTGCC 276
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22667 CCTATCTCTATCATGTACACCCCATCCACATCTCCATCATACATCAACCTCATCCCTATC 22726

Qy 277 TCCGACCAATCCGCGGCCACCAACTGGGTCAAAACCAAGTCCAAAGCTACCCAAACGTT 336
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22727 TCCATCATATACAACCTCCATCTCTCCAAAACATACAACCCCATCCCACTCCCATC 22786

Qy 337 GCCTTCCGATACATCGCGGTGGAAACGAAGTCAATCCCC 375
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22787 ACATAACAACCCATCCCAACCTCCATCATCATGCAACCC 22825

RESULT 15
US-11-114-798-52
; Sequence 52, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 165911
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-52

Query Match          4.2%; Score 47; DB 11; Length 165911;
Best Local Similarity 48.0%; Pred. No. 0.042;
Matches 134; Conservative 0; Mismatches 145; Indels 0; Gaps 0;
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Qy 97 TGCATGAATGGAGCGTGACAACCTCCCGCGCGCGAGCTCGTCAACTCTTACAAAG 156
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131525 TACAACCCCATCCCGCTCTCCATCATGTACAAACCCCATCCCACTCCATCGTGTACAAAC 131584

Qy 157 TCCAAACAATAGCTGGCATCGGACTCTACAGCCCGGACCAAGCACTCTCCAGGCCCTC 216
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131585 CCGATCCCGCTTCCATCATCAGTACAAACCCCATCCCACTCCATCATACATCAACCCCATC 131644

Qy 217 CAGGGCTCTAACATCTACCTCATCTCGAGCTCCCAACTCCGACCTCCAAAACATTTGCC 276
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131645 CCTATCTCTATCATGTACAAACCCCATCCACATCTCCATCATACATCAACCTCATCCCTATC 131704

Qy 277 TCCGACCAATCCGCGGCCACCAACTGGGTCAAAACCAAGTCCAAAGCTACCCAAACGTT 336
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131705 TCCATCATATACAACCTCCATCTCTCCAAAACATACAACCCCATCCCACTCCCATC 131764

Qy 337 GCCTTCCGATACATCGCGGTGGAAACGAAGTCAATCCCC 375
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131765 ACATAACAACCCATCCCAACCTCCATCATCATGCAACCC 131803
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Search completed: April 7, 2006, 22:54:12
Job time : 664 secs